

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 29, 2001, 13:49:17 ; Search time 172.16 Seconds
(without alignments)
746.106 Million cell updates/sec

Title: US-09-466-396A-176

Perfect score: 2956

Sequence: 1 MNKLYIGNLSENAAPSDLES.....VKHQOQKALQSGPPQSRRK 579

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main.*
1: /cgn2_6/ptodata/2/paa/PCRTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2956	100.0	579	18	US-09-466-396A-176
2	2956	100.0	579	19	US-09-542-615A-176
3	2956	100.0	579	20	US-09-606-421A-176
4	2956	100.0	579	20	US-09-630-940A-176
5	2956	100.0	579	20	US-09-643-597-176
6	2956	100.0	579	20	US-09-662-786-176
7	2956	100.0	579	20	US-09-685-696-176
8	2956	100.0	579	20	US-09-735-705-176
9	2956	100.0	579	21	US-09-850-716-176
10	2956	100.0	579	22	US-09-850-716-176

11	2943	99.6	579	19	US-09-542-615A-348	Sequence 348, App
12	2943	99.6	579	20	US-09-606-421A-348	Sequence 348, App
13	2943	99.6	579	20	US-09-630-940A-348	Sequence 348, App
14	2943	99.6	579	20	US-09-630-940B-348	Sequence 348, App
15	2943	99.6	579	20	US-09-643-597-348	Sequence 348, App
16	2943	99.6	579	20	US-09-662-786-348	Sequence 348, App
17	2943	99.6	579	20	US-09-685-696-348	Sequence 348, App
18	2943	99.6	579	21	US-09-735-705-348	Sequence 348, App
19	2943	99.6	579	22	US-09-850-716-348	Sequence 348, App
20	2938	99.4	586	22	US-09-850-716-427	Sequence 427, App
21	1950.5	66.0	603	1	PCT-US01-01307-592	Sequence 592, App
22	1946.5	65.8	620	1	PCT-US01-01341-1116	Sequence 1116, App
23	949	32.1	261	1	PCT-US01-01341-1114	Sequence 1114, App
24	919	31.1	250	1	PCT-US01-01341-1532	Sequence 1532, App
25	896	30.3	1219	23	US-60-161-932-1355	Sequence 1355, App
26	835.5	28.3	558	23	US-60-191-637-1899	Sequence 1899, App
27	835.5	28.3	558	23	US-60-191-681-1524	Sequence 1524, App
28	832.5	28.2	558	23	US-60-167-217-1955	Sequence 1955, App
29	832.5	28.2	558	23	US-60-173-464-1602	Sequence 1602, App
30	626	21.2	171	1	PCT-US01-01341-1119	Sequence 1119, App
31	527	17.8	192	1	PCT-US01-01341-1117	Sequence 1117, App
32	503.5	17.0	136	23	US-60-236-804-688	Sequence 688, App
33	474	16.0	93	1	PCT-US01-00663-38770	Sequence 38770, App
34	437	14.8	144	23	US-60-188-162-2591	Sequence 2591, App
35	402	13.6	171	1	PCT-US01-01341-1536	Sequence 1536, App
36	360.5	12.2	131	1	PCT-US01-01307-848	Sequence 848, App
37	282	9.5	182	23	US-60-146-394-1584	Sequence 1584, App
38	280	9.5	182	23	US-60-143-992-1350	Sequence 1350, App
39	229	7.7	386	23	US-60-167-217-16663	Sequence 16663, App
40	229	7.7	386	23	US-60-173-464-13643	Sequence 13643, App
41	229	7.7	386	23	US-60-191-637-16673	Sequence 16673, App
42	229	7.7	386	23	US-60-191-681-13184	Sequence 13184, App
43	227	7.7	45	1	PCT-US01-00663-37584	Sequence 37584, App
44	226	7.6	1268	23	US-60-167-216-264	Sequence 264, App
45	226	7.6	1268	23	US-60-173-464-8713	Sequence 8713, App

ALIGNMENTS

RESULT 1
US-09-466-396A-176
; Sequence 176, Application US/09466396A
; GENERAL INFORMATION:
; APPLICANT: Wang, TongTong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-396A-176

Query Match 100.0%; Score 2956; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNKLTYGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGTAFAVDCPDSEWALKAIKALSGK	60
Db	1	MNKLTYGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGTAFAVDCPDSEWALKAIKALSGK	60
Qy	61	IELHGKPIEVEHSVPRQRIRKLIQIRNIPPHLQWEVLDLSLLVOYGVVSECEQVNTDSETA	120
Db	61	IELHGKPIEVEHSVPRQRIRKLIQIRNIPPHLQWEVLDLSLLVOYGVVSECEQVNTDSETA	120
Qy	121	VYNTVYSSKQDQARQALDKUNGFOLENTFKVAYIPDEMAQQNPLOQPRGRGLGORGSS	180
Db	121	VYNTVYSSKQDQARQALDKUNGFOLENTFKVAYIPDEMAQQNPLOQPRGRGLGORGSS	180

Db 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180
Qy 181 RQSPGSVSKOKPCDPLRLLLVPTQFVGAIIKKGATIRNITKOTQSKIDVHRKENAGAA 240
Db 181 RQSPGSVSKOKPCDPLRLLLVPTQFVGAIIKKGATIRNITKOTQSKIDVHRKENAGAA 240
Qy 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGKEGRNLK 300
Db 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGKEGRNLK 300
Qy 301 KIEQDTDTKITISPLQELTYLNPRTITVKNVETCAKAEEMKIKRESYENDIASNNL 360
Db 301 KIEQDTDTKITISPLQELTYLNPRTITVKNVETCAKAEEMKIKRESYENDIASNNL 360
Qy 361 QAHLIPGLNLAGLFPPTSGMPPTSGPPSAMTPPYPOFQSETETVHQIPALSVGAI 420
Db 361 QAHLIPGLNLAGLFPPTSGMPPTSGPPSAMTPPYPOFQSETETVHQIPALSVGAI 420
Qy 421 IKGOQHITKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQKAGRIYKIKENFV 480
Db 421 IKGOQHITKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQKAGRIYKIKENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Qy 541 GHFYACQVQAKRIQEIILTVKQHOQKALQSGPPQSRK 579
Db 541 GHFYACQVQAKRIQEIILTVKQHOQKALQSGPPQSRK 579

RESULT 2

US-09-542-615A-176
; Sequence 176, Application US/09542615A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-176

Query Match 100.0%; Score 2956; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDESWALKATEALSGK 60
Db 1 MNKLYIGNLSENAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDESWALKATEALSGK 60
Qy 61 IELHGKPIEVSHSVKQRIRKLRINIPHLQWEVLDSLVLVQGVVSESCQVNTDSETA 120
Db 61 IELHGKPIEVSHSVKQRIRKLRINIPHLQWEVLDSLVLVQGVVSESCQVNTDSETA 120
Qy 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180
Db 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180
Qy 181 RQSPGSVSKOKPCDPLRLLLVPTQFVGAIIKKGATIRNITKOTQSKIDVHRKENAGAA 240

Db 181 RQSPGSVSKOKPCDPLRLLLVPTQFVGAIIKKGATIRNITKOTQSKIDVHRKENAGAA 240
Qy 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGKEGRNLK 300
Db 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGKEGRNLK 300
Qy 301 KIEQDTDTKITISPLQELTYLNPRTITVKNVETCAKAEEMKIKRESYENDIASNNL 360
Db 301 KIEQDTDTKITISPLQELTYLNPRTITVKNVETCAKAEEMKIKRESYENDIASNNL 360
Qy 361 QAHLIPGLNLAGLFPPTSGMPPTSGPPSAMTPPYPOFQSETETVHQIPALSVGAI 420
Db 361 QAHLIPGLNLAGLFPPTSGMPPTSGPPSAMTPPYPOFQSETETVHQIPALSVGAI 420
Qy 421 IKGOQHITKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQKAGRIYKIKENFV 480
Db 421 IKGOQHITKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQKAGRIYKIKENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Qy 541 GHFYACQVQAKRIQEIILTVKQHOQKALQSGPPQSRK 579
Db 541 GHFYACQVQAKRIQEIILTVKQHOQKALQSGPPQSRK 579

RESULT 3

US-09-606-421A-176
; Sequence 176, Application US/09606421A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421A-176

Query Match 100.0%; Score 2956; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDESWALKATEALSGK 60
Db 1 MNKLYIGNLSENAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDESWALKATEALSGK 60
Qy 61 IELHGKPIEVSHSVKQRIRKLRINIPHLQWEVLDSLVLVQGVVSESCQVNTDSETA 120
Db 61 IELHGKPIEVSHSVKQRIRKLRINIPHLQWEVLDSLVLVQGVVSESCQVNTDSETA 120
Qy 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180
Db 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180
Qy 181 RQSPGSVSKOKPCDPLRLLLVPTQFVGAIIKKGATIRNITKOTQSKIDVHRKENAGAA 240
Db 181 RQSPGSVSKOKPCDPLRLLLVPTQFVGAIIKKGATIRNITKOTQSKIDVHRKENAGAA 240

[illegible]

RESULT 4

```

US-09-630-940A-176
;
; Sequence 176, Application US/09630940A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940A
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-630-940A-176

```

Query Match	100.0%;	Score 2956;	DB 20;	Length 579;
Best Local Similarity	100.0%;	Pred. No. 2.8e-243;		
Matches 579;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	MNKLIGNLSENAAPSDLEISIFKDAKIPVSGPFLVKVTGYAFVDCPDDESWALKATEALSCK 60			
Db	1 MNKLIGNLSENAAPSDLEISIFKDAKIPVSGPFLVKVTGYAFVDCPDDESWALKATEALSCK 60			
QY 61	IELHGKPIEVHSHVPKQRIRTKLQIRNIPPHLOWEVLDSLVLVQVGVESCQVNTDSETA 120			
Db	61 IELHGKPIEVHSHVPKQRIRTKLQIRNIPPHLOWEVLDSLVLVQVGVESCQVNTDSETA 120			
QY 121	VVWVTYSSKQOARQALDKLNGFQLENFTLVKAYITPDEMAAQONPLQOPGRRGGLQGRGSS 180			
Db	121 VVWVTYSSKQOARQALDKLNGFQLENFTLVKAYITPDEMAAQONPLQOPGRRGGLQGRGSS 180			
QY 181	RQSGPGSVSKQKPCDLPURLLLVPTQFVGAIIGKKGATIRNITTKQTQSKIDIVHRKENAGAA 240			

Db	181	RQSGPSGVSKQPCDPLRLVPTQFVGALIGKEGATIRNITQOTQSKDVRKENAGAA	240
QY	241	EKSITILSTPEGTSAAACKSILEIMHKEAQDIFTEEIPLKILAHNNFVGRGLIGKEGRNLK	300
Db	241	EKSITILSTPEGTSAAACKSILEIMHKEAQDIFTEEIPLKILAHNNFVGRGLIGKEGRNLK	300
QY	301	KIBQDQTDTKITSPLOBELILYNPERTITVKNGVETCAKAEIEIMKKIRESYENDIASMNL	360
Db	301	KIBQDQTDTKITSPLOBELILYNPERTITVKNGVETCAKAEIEIMKKIRESYENDIASMNL	360
QY	361	QAHILPLGLNLNALGLPPPTSGMPPPTSGPPSAMTPPYPOFEQSESETVTHQFIPALSVGAI	420
Db	361	QAHILPLGLNLNALGLPPPTSGMPPPTSGPPSAMTPPYPOFEQSESETVTHQFIPALSVGAI	420
QY	421	IGKQGOHIKQLSRFACASTIKIAPAEAPDAKVRMVIITGTPPEAQFKAQGRYIGKIKREENPV	480
Db	421	IGKQGOHIKQLSRFACASTIKIAPAEAPDAKVRMVIITGTPPEAQFKAQGRYIGKIKREENPV	480
QY	481	SPKEEVKLEAHIRVPFSFAAGRVIGKGKTKVNLONLSSAEVVVPVPRDQTDENDQVVVKIT	540
Db	481	SPKEEVKLEAHIRVPFSFAAGRVIGKGKTKVNLONLSSAEVVVPVPRDQTDENDQVVVKIT	540
QY	541	GHPYACQVQARKTQETILTQVQHQHQKALQSGPPQSRKK	579
Db	541	GHPYACQVQARKTQETILTQVQHQHQKALQSGPPQSRKK	579

RESULT 5

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RESULTS:
US-09-630-940B-176
; Sequence 176, Application US/09630940B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-630-940B-176

```

	Query Match	100.0%;	Score 2956;	DB 20;	Length 579;		
	Best Local Similarity	100.0%;	Pred. No. 2.8e-243;				
	Matches 579;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1	MNKL	YICNLS	ENAA	PSDLESIFKDAKIPVSGPFLVKTGYAFVDCPD	ESWALKATEALS	SGK 60
Db	1	MNKL	YICNLS	ENAA	PSDLESIFKDAKIPVSGPFLVKTGYAFVDCPD	ESWALKATEALS	SGK 60
QY	61	IELHGKPI	IEVH	SVPKRQIRKQIRNIP	PHLQWEVLDSL	LLVQYGVV	ESCEQVNTDSETA 120
Db	61	IELHGKPI	IEVH	SVPKRQIRKQIRNIP	PHLQWEVLDSL	LLVQYGVV	ESCEQVNTDSETA 120
QY	121	VWNYTSSKQ	QARQALDKL	NGFQLEN	TLKVAYIP	DEMAAQNP	LQOPRGRGLGQRSS 180
Db	121	VWNYTSSKQ	QARQALDKL	NGFQLEN	TLKVAYIP	DEMAAQNP	LQOPRGRGLGQRSS 180
QY	181	ROGSPG	SVSKOKPCDL	PLRLLVPT	OFVTCGAI	IGKRGATIRN	TLTKOTOSKIDVHRKENAGAA 240

```
Db 181 RQSPGVSQKPCDPLRLLLVPTQFVGAIIGKGGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTEETPLKTLAHNNFVGRILIGEGRNK 300
Db 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTEETPLKTLAHNNFVGRILIGEGRNK 300
Qy 301 KIEODTDTKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Db 301 KIEODTDTKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Qy 361 QAHILPGLNUNALGLFPPTSGMPPTSGPPSAMPPTPPYQFQSETEVHQFIPALSVCAL 420
Db 361 QAHILPGLNUNALGLFPPTSGMPPTSGPPSAMPPTPPYQFQSETEVHQFIPALSVCAL 420
Qy 421 IGKOGQHIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQRIYKGIKEENFV 480
Db 421 IGKOGQHIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQRIYKGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQTPDENDQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQTPDENDQVVKIT 540
Qy 541 GHFYACQVAQRKIQEILITQVKHQHQQKALQSGPPQSRKK 579
Db 541 GHFYACQVAQRKIQEILITQVKHQHQQKALQSGPPQSRKK 579
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RESULT 6

```
US-09-643-597-176
; Sequence 176, Application US/09643597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-176
```

```
Query Match 100.0%; Score 2956; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDESIFDKAPIVSGPFLVKTYGAFVDCPDSESWALKAEALSGK 60
Db 1 MNKLYIGNLSENAAPSDESIFDKAPIVSGPFLVKTYGAFVDCPDSESWALKAEALSGK 60
Qy 61 IELHGKPIEVESHVPKQRIRKLRIRNIPHLQWEVLDSLLVQYGVVSCQVNTDSETA 120
Db 61 IELHGKPIEVESHVPKQRIRKLRIRNIPHLQWEVLDSLLVQYGVVSCQVNTDSETA 120
Qy 121 VVNTYSSKQDQARQALDKLNGFLENFTLKVAYIPDEMAAQNPLOQPRGRRLGQGRSS 180
Db 121 VVNTYSSKQDQARQALDKLNGFLENFTLKVAYIPDEMAAQNPLOQPRGRRLGQGRSS 180
```

```
Qy 181 RQSPGVSQKPCDPLRLLLVPTQFVGAIIGKGGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGVSQKPCDPLRLLLVPTQFVGAIIGKGGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTEETPLKTLAHNNFVGRILIGEGRNK 300
Db 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTEETPLKTLAHNNFVGRILIGEGRNK 300
Qy 301 KIEODTDTKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Db 301 KIEODTDTKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Qy 361 QAHILPGLNUNALGLFPPTSGMPPTSGPPSAMPPTPPYQFQSETEVHQFIPALSVCAL 420
Db 361 QAHILPGLNUNALGLFPPTSGMPPTSGPPSAMPPTPPYQFQSETEVHQFIPALSVCAL 420
Qy 421 IGKOGQHIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQRIYKGIKEENFV 480
Db 421 IGKOGQHIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQRIYKGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQTPDENDQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQTPDENDQVVKIT 540
Qy 541 GHFYACQVAQRKIQEILITQVKHQHQQKALQSGPPQSRKK 579
Db 541 GHFYACQVAQRKIQEILITQVKHQHQQKALQSGPPQSRKK 579
```

RESULT 7

```
US-09-662-786-176
; Sequence 176, Application US/09662786
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C12
; CURRENT APPLICATION NUMBER: US/09/662.786
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-662-786-176
```

```
Query Match 100.0%; Score 2956; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDESIFDKAPIVSGPFLVKTYGAFVDCPDSESWALKAEALSGK 60
Db 1 MNKLYIGNLSENAAPSDESIFDKAPIVSGPFLVKTYGAFVDCPDSESWALKAEALSGK 60
Qy 61 IELHGKPIEVESHVPKQRIRKLRIRNIPHLQWEVLDSLLVQYGVVSCQVNTDSETA 120
Db 61 IELHGKPIEVESHVPKQRIRKLRIRNIPHLQWEVLDSLLVQYGVVSCQVNTDSETA 120
Qy 121 VVNTYSSKQDQARQALDKLNGFLENFTLKVAYIPDEMAAQNPLOQPRGRRLGQGRSS 180
Db 121 VVNTYSSKQDQARQALDKLNGFLENFTLKVAYIPDEMAAQNPLOQPRGRRLGQGRSS 180
```


QY 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
DB 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
QY 241 EKSITILSTPETSAAKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
DB 241 EKSITILSTPETSAAKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
QY 301 KIEQDTRKTIPTISPLQELTLYNPRTITVKGNVETCAKAEIEIMKKIRIESYENDIASMNL 360
DB 301 KIEQDTRKTIPTISPLQELTLYNPRTITVKGNVETCAKAEIEIMKKIRIESYENDIASMNL 360
QY 361 QAHLLPGLNLNAGLFPPTSGMPPTSGPPSAMPPTPYQFQSETETVHQFIPALSUGAI 420
DB 361 QAHLLPGLNLNAGLFPPTSGMPPTSGPPSAMPPTPYQFQSETETVHQFIPALSUGAI 420
QY 421 TKQOQHILKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQRIYKIKEENFV 480
DB 421 TKQOQHILKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQRIYKIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
QY 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579
DB 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579

RESULT 8

US-09-685-696-176

; Sequence 176, Application US/09685696
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C13
; CURRENT APPLICATION NUMBER: US/09/685,696
; CURRENT FILING DATE: 2000-10-09
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-696-176

Query Match 100.0%; Score 2956; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSGK 60
QY 61 IELHGKPIEVEHSVPRQIRKIQIRNIPPHLQWEVDSLLVQYGVWESCEQVNTDSETA 120
DB 61 IELHGKPIEVEHSVPRQIRKIQIRNIPPHLQWEVDSLLVQYGVWESCEQVNTDSETA 120
QY 121 VVNVITYSSKDOARQALDKINGFOLENFTLKVAYIDEMAQONPQQPRGRGLQORSS 180
DB 121 VVNVITYSSKDOARQALDKINGFOLENFTLKVAYIDEMAQONPQQPRGRGLQORSS 180

DB 121 VVNVITYSSKDOARQALDKINGFOLENFTLKVAYIDEMAQONPQQPRGRGLQORSS 180
QY 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
DB 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
QY 241 EKSITILSTPETSAAKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
DB 241 EKSITILSTPETSAAKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
QY 301 KIEQDTRKTIPTISPLQELTLYNPRTITVKGNVETCAKAEIEIMKKIRIESYENDIASMNL 360
DB 301 KIEQDTRKTIPTISPLQELTLYNPRTITVKGNVETCAKAEIEIMKKIRIESYENDIASMNL 360
QY 361 QAHLLPGLNLNAGLFPPTSGMPPTSGPPSAMPPTPYQFQSETETVHQFIPALSUGAI 420
DB 361 QAHLLPGLNLNAGLFPPTSGMPPTSGPPSAMPPTPYQFQSETETVHQFIPALSUGAI 420
QY 421 TKQOQHILKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQRIYKIKEENFV 480
DB 421 TKQOQHILKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQRIYKIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
QY 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579
DB 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579

RESULT 9

US-09-735-705-176

; Sequence 176, Application US/09735705
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-176

Query Match 100.0%; Score 2956; DB 21; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSGK 60
QY 61 IELHGKPIEVEHSVPRQIRKIQIRNIPPHLQWEVDSLLVQYGVWESCEQVNTDSETA 120
DB 61 IELHGKPIEVEHSVPRQIRKIQIRNIPPHLQWEVDSLLVQYGVWESCEQVNTDSETA 120

```
QY 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRGRGLGQRSS 180
DB 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRGRGLGQRSS 180
QY 181 ROGSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKTQSKIDVHRKENAGAA 240
DB 181 ROGSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKTQSKIDVHRKENAGAA 240
QY 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGEGRNK 300
DB 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGEGRNK 300
QY 301 KIEODTDTKITISPLQELTYLNPERTITVKGNETCAKAEIIMKKIRESYENDIASNNL 360
DB 301 KIEODTDTKITISPLQELTYLNPERTITVKGNETCAKAEIIMKKIRESYENDIASNNL 360
QY 361 QAHLPGLNALGLFPPTSGMPPTSGPPSAMTPPYQPEQSETEVHQIPALSVAI 420
DB 361 QAHLPGLNALGLFPPTSGMPPTSGPPSAMTPPYQPEQSETEVHQIPALSVAI 420
QY 421 IGKQGHQIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
DB 421 IGKQGHQIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVVPRDQTPDENQDVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVVPRDQTPDENQDVVVKIT 540
QY 541 GHFYACQVAQRKIQEILTVQKHQOQKALQSGPPQSRKK 579
DB 541 GHFYACQVAQRKIQEILTVQKHQOQKALQSGPPQSRKK 579
```

RESULT 10

```
US-09-850-716-176
; Sequence 176, Application US/09850716
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fangert, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fangert, Neil
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716-176
```

```
Query Match 100.0%; Score 2956; DB 22; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSENAAPSDLESIFDKAKIPVSGPFLVKTYAFVDCPDSEWALKATEALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFDKAKIPVSGPFLVKTYAFVDCPDSEWALKATEALSGK 60
QY 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLQVGVVSCQVNTDSETA 120
```

```
DB 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLQVGVVSCQVNTDSETA 120
QY 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRGRGLGQRSS 180
DB 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRGRGLGQRSS 180
QY 181 ROGSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKTQSKIDVHRKENAGAA 240
DB 181 ROGSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKTQSKIDVHRKENAGAA 240
QY 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGEGRNK 300
DB 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGEGRNK 300
QY 301 KIEODTDTKITISPLQELTYLNPERTITVKGNETCAKAEIIMKKIRESYENDIASNNL 360
DB 301 KIEODTDTKITISPLQELTYLNPERTITVKGNETCAKAEIIMKKIRESYENDIASNNL 360
QY 361 QAHLPGLNALGLFPPTSGMPPTSGPPSAMTPPYQPEQSETEVHQIPALSVAI 420
DB 361 QAHLPGLNALGLFPPTSGMPPTSGPPSAMTPPYQPEQSETEVHQIPALSVAI 420
QY 421 IGKQGHQIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
DB 421 IGKQGHQIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVVPRDQTPDENQDVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVVPRDQTPDENQDVVVKIT 540
QY 541 GHFYACQVAQRKIQEILTVQKHQOQKALQSGPPQSRKK 579
DB 541 GHFYACQVAQRKIQEILTVQKHQOQKALQSGPPQSRKK 579
```

RESULT 11

```
US-09-542-615A-348
; Sequence 348, Application US/09542615A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fangert, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-348
```

```
Query Match 99.6%; Score 2943; DB 19; Length 579;
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSENAAPSDLESIFDKAKIPVSGPFLVKTYAFVDCPDSEWALKATEALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFDKAKIPVSGPFLVKTYAFVDCPDSEWALKATEALSGK 60
QY 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLQVGVVSCQVNTDSETA 120
DB 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLQVGVVSCQVNTDSETA 120
QY 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRGRGLGQRSS 180
```

```
Db 121 VVNTYSSKQARQALDKLNGFLENFTLKVAYIDPETAQONPLQQPRGRGLGQSS 180
Qy 181 RQSPGSYSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGSYSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSITILSTPSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Db 241 EKSITILSTPSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Qy 301 KIEQDTRKITISPLQELTLYNPERTITVKGNVETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEQDTRKITISPLQELTLYNPERTITVKGNVETCAKAEIEIMKKIRESYENDIASMNL 360
Qy 361 QAHLLPGLNLNALGLFPPTSGMPPPTSGPPSAMPPTPYQFQESQSETETVHQFIPALSVGAI 420
Db 361 QAHLLPGLNLNALGLFPPTSGMPPPTSGPPSAMPPTPYQFQESQSETETVHLFIPALSVGAI 420
Qy 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQFKAQGRYIKKEENFV 480
Db 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQFKAQGRYIKKEENFV 480
Qy 481 SPKEVKLEAHLIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Db 481 SPKEVKLEAHLIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Qy 541 GHFYACQVAQRKIQEILTQVKHQHQQKALQSGPPQSRRK 579
Db 541 GHFYACQVAQRKIQEILTQVKHQHQQKALQSGPPQSRRK 579
```

RESULT 12

```
US-09-606-421A-348
; Sequence 348, Application US/09606421A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421A-348
```

```
Query Match 99.6%; Score 2943; DB 20; Length 579;
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 MNKLYIGNLSENAAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSCK 60
Db 1 MNKLYIGNLSENAAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSCK 60
Qy 61 IELHGKPIEVEHSVPKQRIKRLQIRNIPPHLQWEVLDLSLLVQYGVWESCEQVNTDSETA 120
Db 61 IELHGKPIEVEHSVPKQRIKRLQIRNIPPHLQWEVLDLSLLVQYGVWESCEQVNTDSETA 120
Qy 121 VVNTYSSKQARQALDKLNGFLENFTLKVAYIDPETAQONPLQQPRGRGLGQSS 180
```

```
Db 121 VVNTYSSKQARQALDKLNGFLENFTLKVAYIDPETAQONPLQQPRGRGLGQSS 180
Qy 181 RQSPGSYSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGSYSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSITILSTPSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Db 241 EKSITILSTPSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Qy 301 KIEQDTRKITISPLQELTLYNPERTITVKGNVETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEQDTRKITISPLQELTLYNPERTITVKGNVETCAKAEIEIMKKIRESYENDIASMNL 360
Qy 361 QAHLLPGLNLNALGLFPPTSGMPPPTSGPPSAMPPTPYQFQESQSETETVHQFIPALSVGAI 420
Db 361 QAHLLPGLNLNALGLFPPTSGMPPPTSGPPSAMPPTPYQFQESQSETETVHLFIPALSVGAI 420
Qy 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQFKAQGRYIKKEENFV 480
Db 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQFKAQGRYIKKEENFV 480
Qy 481 SPKEVKLEAHLIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Db 481 SPKEVKLEAHLIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Qy 541 GHFYACQVAQRKIQEILTQVKHQHQQKALQSGPPQSRRK 579
Db 541 GHFYACQVAQRKIQEILTQVKHQHQQKALQSGPPQSRRK 579
```

RESULT 13

```
US-09-630-940A-348
; Sequence 348, Application US/09630940A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630.940A
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-630-940A-348
```

```
Query Match 99.6%; Score 2943; DB 20; Length 579;
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 MNKLYIGNLSENAAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSCK 60
Db 1 MNKLYIGNLSENAAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSCK 60
Qy 61 IELHGKPIEVEHSVPKQRIKRLQIRNIPPHLQWEVLDLSLLVQYGVWESCEQVNTDSETA 120
Db 61 IELHGKPIEVEHSVPKQRIKRLQIRNIPPHLQWEVLDLSLLVQYGVWESCEQVNTDSETA 120
Qy 121 VVNTYSSKQARQALDKLNGFLENFTLKVAYIDPETAQONPLQQPRGRGLGQSS 180
```

```
Db 121 VVNTYSSKQARQALDKLNGFLENFTLVAYIPDETAQAQNPLOQPRGRRLGQRGSS 180
Qy 181 RQSPGVSQKQPCDPLRLLLVPTQFVCAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGVSQKQPCDPLRLLLVPTQFVCAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRIGKEGRNLK 300
Db 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRIGKEGRNLK 300
Qy 301 KIEQDTFKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Db 301 KIEQDTFKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Qy 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVCAL 420
Db 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVCAL 420
Qy 421 IGKQGHKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQKAGRIYKGIKEENFV 480
Db 421 IGKQGHKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQKAGRIYKGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENQVVKIT 540
Qy 541 GHFYACQVAQRKIQEILTVQKHQOQKALQSGPPQSRKK 579
Db 541 GHFYACQVAQRKIQEILTVQKHQOQKALQSGPPQSRKK 579
```

RESULT 14

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US-09-630-940B-348
; Sequence 348, Application US/09630940B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-630-940B-348
```

```
Query Match 99.6%; Score 2943; DB 20; Length 579;
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAPSDLESIFDKAKIPVSGPFLVKTYGAFVDCPDSESWALKATEALSGK 60
Db 1 MNKLYIGNLSENAPSDLESIFDKAKIPVSGPFLVKTYGAFVDCPDSESWALKATEALSGK 60
Qy 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLVLQYGVVESCQVNTDSETA 120
Db 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLVLQYGVVESCQVNTDSETA 120
```

```
Qy 121 VVNTYSSKQARQALDKLNGFLENFTLVAYIPDEMAQAQNPLOQPRGRRLGQRGSS 180
Db 121 VVNTYSSKQARQALDKLNGFLENFTLVAYIPDETAQAQNPLOQPRGRRLGQRGSS 180
Qy 181 RQSPGVSQKQPCDPLRLLLVPTQFVCAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGVSQKQPCDPLRLLLVPTQFVCAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRIGKEGRNLK 300
Db 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRIGKEGRNLK 300
Qy 301 KIEQDTFKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Db 301 KIEQDTFKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Qy 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVCAL 420
Db 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVCAL 420
Qy 421 IGKQGHKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQKAGRIYKGIKEENFV 480
Db 421 IGKQGHKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQKAGRIYKGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENQVVKIT 540
Qy 541 GHFYACQVAQRKIQEILTVQKHQOQKALQSGPPQSRKK 579
Db 541 GHFYACQVAQRKIQEILTVQKHQOQKALQSGPPQSRKK 579
```

RESULT 15

```
US-09-643-597-348
; Sequence 348, Application US/09643597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-348
```

```
Query Match 99.6%; Score 2943; DB 20; Length 579;
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 MNKLYIGNLSENAPSDLESIFDKAKIPVSGPFLVKTYGAFVDCPDSESWALKATEALSGK 60
Db 1 MNKLYIGNLSENAPSDLESIFDKAKIPVSGPFLVKTYGAFVDCPDSESWALKATEALSGK 60
Qy 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLVLQYGVVESCQVNTDSETA 120
Db 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLVLQYGVVESCQVNTDSETA 120
```

Qy	121	VNVYSSKDDQARQALDKLNGFQLENFTLKVAYIPDEMAAQONPLQOPRRRGLGQRGSS	180
Db	121	VNVYSSKDDQARQALDKLNGFQLENFTLKVAYIPDETAQONPLQOPRRRGLGQRGSS	180
Qy	181	ROSGPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA	240
Db	181	ROSGPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA	240
Qy	241	EKSITILSTPETSAAKCSILEIMHKEAQDIKFTTEEIPLKILAHNNFVGRLLIGKEGRNLK	300
Db	241	EKSITILSTPETSAAKCSILEIMHKEAQDIKFTTEEIPLKILAHNNFVGRLLIGKEGRNLK	300
Qy	301	KIEQDQTKITISPLQELTYNPERTITVKGNVETCAKAEIEIMKKIRESYENDIASMNL	360
Db	301	KIEQDQTKITISPLQELTYNPERTITVKGNVETCAKAEIEIMKKIRESYENDIASMNL	360
Qy	361	QAHLLPGLNLALGLFPPTSGMPPPTSGPPSAMTPPYPOFQSETEHVHOFIPALSVGAI	420
Db	361	QAHLLPGLNLALGLFPPTSGMPPPTSGPPSAMTPPYPOFQSETEHVHOFIPALSVGAI	420
Qy	421	ICKQGOHIKQLSRFAGASTIKIAPAEAPDAKVRMVIITGPPEAQKAGRIYGIKEENFV	480
Db	421	ICKQGOHIKQLSRFAGASTIKIAPAEAPDAKVRMVIITGPPEAQKAGRIYGIKEENFV	480
Qy	481	SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT	540
Db	481	SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT	540
Qy	541	GHFYACQVAORKIOEILLTOVKOHQOQKALQSGPPQSRRK	579
Db	541	GHFYACQVAORKIOEILLTOVKOHQOQKALQSGPPQSRRK	579

Search completed: September 29, 2001, 13:59:28
Job time: 611 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 29, 2001, 13:53:37 ; Search time 358.89 Seconds
(without alignments)
71.651 Million cell updates/sec

Title: US-09-466-396A-176
Perfect score: 2956
Sequence: 1 MNKLYIGNLSNAAPSDLES.....VKHQKQKALQSGPPQSRRK 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 285759 seqs, 44412722 residues

Total number of hits satisfying chosen parameters: 285759

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2956	100.0	579	US-09-897-778-176	Sequence 176, App
2	2956	100.0	579	US-09-510-376A-176	Sequence 176, App
3	2943	99.6	579	US-09-897-778-348	Sequence 348, App
4	2943	99.6	579	US-09-897-778-446	Sequence 446, App
5	2943	99.6	579	US-09-897-778-449	Sequence 449, App
6	2938	99.4	586	US-09-897-778-427	Sequence 427, App
7	2814	95.2	619	PCT-US01-08631-52322	Sequence 52322, A
8	2733	92.5	583	PCT-US01-08631-42951	Sequence 42951, A
9	2190	74.1	577	US-09-873-637-2	Sequence 2, Appl
10	1950.5	66.0	614	PCT-US01-08631-37153	Sequence 37153, A
11	1946.5	65.8	620	US-09-764-864-1116	Sequence 1116, A
12	1868	63.2	594	PCT-US01-08631-37154	Sequence 37154, A
13	1512	51.2	334	US-09-760-466-1096	Sequence 1096, App
14	949	32.1	261	US-09-764-864-1114	Sequence 1114, App
15	919	31.1	250	US-09-764-864-1332	Sequence 1332, App
16	776.5	26.3	209	PCT-US01-08631-52320	Sequence 52320, A
17	775.5	26.2	266	PCT-US01-08631-42952	Sequence 42952, A
18	626	21.2	171	US-09-764-864-1119	Sequence 1119, App
19	551	18.6	148	PCT-US01-08631-52321	Sequence 52321, A
20	543	18.4	132	US-09-760-466-1532	Sequence 1532, App
21	527	17.8	192	US-09-764-864-1117	Sequence 1117, App
22	474	16.0	93	US-09-864-761-48606	Sequence 48606, A
23	402	13.6	171	US-09-764-864-1536	Sequence 1536, App
24	238	8.1	49	US-09-873-637-22	Sequence 22, Appl
25	237	8.0	48	US-09-873-637-24	Sequence 24, Appl
26	232	7.8	49	US-09-873-637-18	Sequence 18, Appl
27	229.5	7.8	627	US-09-760-466-1091	Sequence 1091, App

28	229	7.7	571	1	PCT-US01-14826-341	Sequence 341, App
29	227	7.7	45	5	US-09-864-761-45987	Sequence 45987, A
30	227	7.7	47	5	US-09-873-637-23	Sequence 23, Appl
31	225	7.6	47	5	US-09-873-637-21	Sequence 21, Appl
32	222	7.5	479	5	US-09-573-655A-405	Sequence 405, App
33	222	7.5	479	5	US-09-573-655A-1593	Sequence 1593, App
34	219	7.4	48	5	US-09-873-637-20	Sequence 20, Appl
35	218	7.4	47	5	US-09-873-637-17	Sequence 17, Appl
36	217	7.4	507	1	PCT-US01-08631-53601	Sequence 53601, A
37	217	7.3	574	6	US-60-312-544-9800	Sequence 9800, App
38	214	7.2	542	5	US-09-760-466-1523	Sequence 1523, App
39	214	7.2	584	5	US-09-760-466-1081	Sequence 1081, App
40	210	7.1	371	5	US-09-760-466-1090	Sequence 1090, App
41	207.5	7.0	1268	5	US-09-538-092-1235	Sequence 1235, App
42	207.5	7.0	1310	1	PCT-US01-08656-9457	Sequence 9457, App
43	195.5	6.6	522	5	US-09-760-466-1084	Sequence 1084, App
44	190	6.4	47	5	US-09-873-637-19	Sequence 19, Appl
45	190	6.4	466	5	US-09-760-466-1095	Sequence 1095, App

ALIGNMENTS

RESULT 1
US-09-897-778-176
; Sequence 176, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-176

Query Match	100.0%	Score	2956;	DB	5;	Length	579;
Best Local Similarity	100.0%	Pred. No.	1e-195;				
Matches	579;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MNKLTYIGNLSNAAPSDLESIFKDAKIPVSGPFLVKTGTAFVDCPDSEWALKAI	SGK	60			
Db	1	MNKLTYIGNLSNAAPSDLESIFKDAKIPVSGPFLVKTGTAFVDCPDSEWALKAI	SGK	60			
QY	61	IELHGKPIEVEHSVPRKRIKQIRNIPHLQWEVLDSLLVOYGVVESCQVNTDSETA	120				
Db	61	IELHGKPIEVEHSVPRKRIKQIRNIPHLQWEVLDSLLVOYGVVESCQVNTDSETA	120				
QY	121	VNVVTVSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLOQPRGRRLG	RGSS	180			
Db	121	VNVVTVSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLOQPRGRRLG	RGSS	180			
QY	181	RQSGPSVSKQPCDPLRLLLVPTQFVGALIGKEGATIRNITKOTSKIDVHRKENA	GAA	240			
Db	181	RQSGPSVSKQPCDPLRLLLVPTQFVGALIGKEGATIRNITKOTSKIDVHRKENA	GAA	240			
QY	241	EKSITILSPETGTSACKSILEIMHKEAQDIKFTTEPIPLKILAHNNFVGLICKE	GNLK	300			
Db	241	EKSITILSPETGTSACKSILEIMHKEAQDIKFTTEPIPLKILAHNNFVGLICKE	GNLK	300			

Qy 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Qy 361 QAHLLPGLNLNAGLFPPTSGMPPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVGAI 420
Db 361 QAHLLPGLNLNAGLFPPTSGMPPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVGAI 420
Qy 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQKAGRIYKGIKEENFV 480
Db 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQKAGRIYKGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGTVNELQNLSSAEVVVPRDQTPDENQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGTVNELQNLSSAEVVVPRDQTPDENQVVKIT 540
Qy 541 GHFYACQVAQRKIOBILTVKHQHQOQKALQSGPPQSRK 579
Db 541 GHFYACQVAQRKIOBILTVKHQHQOQKALQSGPPQSRK 579

RESULT 2

US-09-510-376A-176
; Sequence 176, Application US/09510376A

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C7
; CURRENT APPLICATION NUMBER: US/09/510.376A
; CURRENT FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-510-376A-176

Query Match 100.0%; Score 2956; DB 5; Length 579;
Best Local Similarity 100.0%; Pred. No. 1e-195;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSGK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSGK 60
Qy 61 IELHGKPIEVSHVPKRIKRIKQIRNIPPHLOWEVLDSLLVOYGVVESCQVNTDSETA 120
Db 61 IELHGKPIEVSHVPKRIKRIKQIRNIPPHLOWEVLDSLLVOYGVVESCQVNTDSETA 120
Qy 121 VVNTYSSKQDQARQALDKLNGFQLENFTLVKVIYIPDEMAAQNPLOQPRGRGLGQSGSS 180
Db 121 VVNTYSSKQDQARQALDKLNGFQLENFTLVKVIYIPDEMAAQNPLOQPRGRGLGQSGSS 180
Qy 181 RQSPGVSYSKQKPCDLPURLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGVSYSKQKPCDLPURLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSTILTSTPGTSAACKSILEIMHKAQDIFKTEIPLKILAHNNFVGRILIGEGRNK 300
Db 241 EKSTILTSTPGTSAACKSILEIMHKAQDIFKTEIPLKILAHNNFVGRILIGEGRNK 300
Qy 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360

Qy 361 QAHLLPGLNLNAGLFPPTSGMPPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVGAI 420
Db 361 QAHLLPGLNLNAGLFPPTSGMPPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVGAI 420
Qy 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQKAGRIYKGIKEENFV 480
Db 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQKAGRIYKGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGTVNELQNLSSAEVVVPRDQTPDENQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGTVNELQNLSSAEVVVPRDQTPDENQVVKIT 540
Qy 541 GHFYACQVAQRKIOBILTVKHQHQOQKALQSGPPQSRK 579
Db 541 GHFYACQVAQRKIOBILTVKHQHQOQKALQSGPPQSRK 579

RESULT 3

US-09-897-778-348

; Sequence 348, Application US/09897778

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897.778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348

Query Match 99.6%; Score 2943; DB 5; Length 579;
Best Local Similarity 99.7%; Pred. No. 8.1e-195;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSGK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSGK 60
Qy 61 IELHGKPIEVSHVPKRIKRIKQIRNIPPHLOWEVLDSLLVOYGVVESCQVNTDSETA 120
Db 61 IELHGKPIEVSHVPKRIKRIKQIRNIPPHLOWEVLDSLLVOYGVVESCQVNTDSETA 120
Qy 121 VVNTYSSKQDQARQALDKLNGFQLENFTLVKVIYIPDEMAAQNPLOQPRGRGLGQSGSS 180
Db 121 VVNTYSSKQDQARQALDKLNGFQLENFTLVKVIYIPDEMAAQNPLOQPRGRGLGQSGSS 180
Qy 181 RQSPGVSYSKQKPCDLPURLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGVSYSKQKPCDLPURLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSTILTSTPGTSAACKSILEIMHKAQDIFKTEIPLKILAHNNFVGRILIGEGRNK 300
Db 241 EKSTILTSTPGTSAACKSILEIMHKAQDIFKTEIPLKILAHNNFVGRILIGEGRNK 300
Qy 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Qy 361 QAHLLPGLNLNAGLFPPTSGMPPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVGAI 420

Db 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420
QY 421 IKQGOHIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRYIGKKEENFV 480
Db 421 IKQGOHIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRYIGKKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELONLSSAEVVVPRDQTPDENDQVVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELONLSSAEVVVPRDQTPDENDQVVVKIT 540
QY 541 GHFYACQVAORKIQLTQVKOHQOKALQSGPPQSRRK 579
Db 541 GHFYACQVAORKIQLTQVKOHQOKALQSGPPQSRRK 579

RESULT 4
US-09-897-778-446
; Sequence 446, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-446

Query Match 99.6%; Score 2943; DB 5; Length 579;
Best Local Similarity 99.7%; Pred. No. 8.1e-195;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCK 60
QY 61 IELHGKPIEVEHSVPRQRIRKLIQIRNIPPHLQWEVLDLSLLVQYGVVSECEQVNTDSETA 120
Db 61 IELHGKPIEVEHSVPRQRIRKLIQIRNIPPHLQWEVLDLSLLVQYGVVSECEQVNTDSETA 120
QY 121 VNVVTSSKDOARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRRLGQSGSS 180
Db 121 VNVVTSSKDOARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRRLGQSGSS 180
QY 181 ROGSPGSVKQKPCDPLRLVPTQFVGALIGKEGATIRNITKOTOSKIDVHRKENAGAA 240
Db 181 ROGSPGSVKQKPCDPLRLVPTQFVGALIGKEGATIRNITKOTOSKIDVHRKENAGAA 240
QY 241 EKSITILSTPEGTSAAKSSILEIMHKEAQDIKFTTEIPLKILAHNNFVGLIGKEGRNLK 300
Db 241 EKSITILSTPEGTSAAKSSILEIMHKEAQDIKFTTEIPLKILAHNNFVGLIGKEGRNLK 300
QY 301 KIEQDQDTKITISPLQELTYLPNERTITVKGNVETCAKAEETIMKKIRESYENDIASMNL 360
Db 301 KIEQDQDTKITISPLQELTYLPNERTITVKGNVETCAKAEETIMKKIRESYENDIASMNL 360
QY 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420

Db 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420
QY 421 IKQGOHIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRYIGKKEENFV 480
Db 421 IKQGOHIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRYIGKKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELONLSSAEVVVPRDQTPDENDQVVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELONLSSAEVVVPRDQTPDENDQVVVKIT 540
QY 541 GHFYACQVAORKIQLTQVKOHQOKALQSGPPQSRRK 579
Db 541 GHFYACQVAORKIQLTQVKOHQOKALQSGPPQSRRK 579

RESULT 5
US-09-897-778-449
; Sequence 449, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-449

Query Match 99.6%; Score 2943; DB 5; Length 579;
Best Local Similarity 99.7%; Pred. No. 8.1e-195;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCK 60
QY 61 IELHGKPIEVEHSVPRQRIRKLIQIRNIPPHLQWEVLDLSLLVQYGVVSECEQVNTDSETA 120
Db 61 IELHGKPIEVEHSVPRQRIRKLIQIRNIPPHLQWEVLDLSLLVQYGVVSECEQVNTDSETA 120
QY 121 VNVVTSSKDOARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRRLGQSGSS 180
Db 121 VNVVTSSKDOARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRRLGQSGSS 180
QY 181 ROGSPGSVKQKPCDPLRLVPTQFVGALIGKEGATIRNITKOTOSKIDVHRKENAGAA 240
Db 181 ROGSPGSVKQKPCDPLRLVPTQFVGALIGKEGATIRNITKOTOSKIDVHRKENAGAA 240
QY 241 EKSITILSTPEGTSAAKSSILEIMHKEAQDIKFTTEIPLKILAHNNFVGLIGKEGRNLK 300
Db 241 EKSITILSTPEGTSAAKSSILEIMHKEAQDIKFTTEIPLKILAHNNFVGLIGKEGRNLK 300
QY 301 KIEQDQDTKITISPLQELTYLPNERTITVKGNVETCAKAEETIMKKIRESYENDIASMNL 360
Db 301 KIEQDQDTKITISPLQELTYLPNERTITVKGNVETCAKAEETIMKKIRESYENDIASMNL 360
QY 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420
Db 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420

Qy 421 IGKQGHKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKGIKEENFV 480
Db 421 IGKQGHKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKGIKEENFV 480
Qy 481 SPKEVKLEAHIRVPSFAAGRVIGKGGKTVELQNLSSAEVVPDQTPDENDQVVKIT 540
Db 481 SPKEVKLEAHIRVPSFAAGRVIGKGGKTVELQNLSSAEVVPDQTPDENDQVVKIT 540
Qy 541 GHYACQVAQRKIQELITOVKHOQKQKALQSGPPQSRRK 579
Db 541 GHYACQVAQRKIQELITOVKHOQKQKALQSGPPQSRRK 579

RESULT 6

US-09-897-778-427

; Sequence 427, Application US/09897778

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C16

; CURRENT APPLICATION NUMBER: US/09/897,778

; CURRENT FILING DATE: 2001-06-28

; NUMBER OF SEQ ID NOS: 467

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 427

; LENGTH: 586

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-897-778-427

Query Match 99.48; Score 2938; DB 5; Length 586;
Best Local Similarity 99.78; Pred. No. 1.8e-194;
Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NKLKYLGNLSENAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCKI 61
Db 9 NKLKYLGNLSENAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCKI 68
Qy 62 ELHGKPIEVESHVPKQRIKRLQIRNIPPHLQWEVLDLVLVOYGVVSCQVNTDSETAV 121
Db 69 ELHGKPIEVESHVPKQRIKRLQIRNIPPHLQWEVLDLVLVOYGVVSCQVNTDSETAV 128
Qy 122 VNVYSSKQDQARQALDKLNGFQLENFTLKVAYIDEMAQONPQQPRGRGLGQSSR 181
Db 129 VNVYSSKQDQARQALDKLNGFQLENFTLKVAYIDEMAQONPQQPRGRGLGQSSR 188
Qy 182 QGSPGVSQKQPCDPLRLVPTQFVGAIGKEGATIRNITKQTSKIDVHRKENAGAAE 241
Db 189 QGSPGVSQKQPCDPLRLVPTQFVGAIGKEGATIRNITKQTSKIDVHRKENAGAAE 248
Qy 242 KSITILSTPETSAAKSILSILMHKEAQDIKFTTEIPLKILAHNNFVGRLLGKGRNKK 301
Db 249 KSITILSTPETSAAKSILSILMHKEAQDIKFTTEIPLKILAHNNFVGRLLGKGRNKK 308
Qy 302 LEQDTRKTIISPLQELTLYNPRTITVKGNVETCAKAEIEIMKKIRESYENDIASNMQ 361
Db 309 LEQDTRKTIISPLQELTLYNPRTITVKGNVETCAKAEIEIMKKIRESYENDIASNMQ 368
Qy 362 AHLIPGLNLALGLFPPTSGMPPTSGPPSANTPPYQFQESQETETVHOFTPALSVGAIL 421
Db 369 AHLIPGLNLALGLFPPTSGMPPTSGPPSANTPPYQFQESQETETVHOFTPALSVGAIL 428

Qy 422 GKQGHKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKGIKEENFV 481
Db 429 GKQGHKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKGIKEENFV 488
Qy 482 PKEEVKLEAHIRVPSFAAGRVIGKGGKTVELQNLSSAEVVPDQTPDENDQVVKITG 541
Db 489 PKEEVKLEAHIRVPSFAAGRVIGKGGKTVELQNLSSAEVVPDQTPDENDQVVKITG 548
Qy 542 HFYACQVAQRKIQELITOVKHOQKQKALQSGPPQSRRK 579
Db 549 HFYACQVAQRKIQELITOVKHOQKQKALQSGPPQSRRK 586

RESULT 7
PCT-US01-08631-52322
; Sequence 52322, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 52322
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (542)...(554)
; OTHER INFORMATION: KH domain proteins family of RNA binding proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number PF00013, p-value=1.000
; OTHER INFORMATION: raw score of 5.78
; NAME/KEY: DOMAIN
; LOCATION: (244)...(587)
; OTHER INFORMATION: KH domain identified by Pfam, accession name KH-domain, E-
; OTHER INFORMATION: value=1.5e-41, Pfam score of 151.5
; NAME/KEY: misc_feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-52322

Query Match 95.28; Score 2814; DB 1; Length 619;

Best Local Similarity 95.08; Pred. No. 6.8e-186;

Matches 554; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

Qy 1 MNKLYIGNLSENAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCKI 60
Db 37 MNKLYIGNLSENAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCKI 96
Qy 61 IELHGKPIEVESHVPKQRIKRLQIRNIPPHLQWEVLDLVLVOYGVVSCQVNTDSETA 120
Db 97 IELHGKPIEVESHVPKQRIKRLQIRNIPPHLQWEVLDLVLVOYGVVSCQVNTDSETA 156
Qy 121 VNVYSSKQDQARQALDKLNGFQLENFTLKVAYIDEMAQONPQQPRGRGLGQ 176
Db 157 VNVYSSKQDQARQALDKLNGFQLENFTLKVAYIDEMAQONPQQPRGRGLGQ 216
Qy 177 RGSRSQSGVSQKQPCDPLRLVPTQFVGAIGKEGATIRNITKQTSKIDVHRKEN 236
Db 217 RGSRSQSGVSQKQPCDPLRLVPTQFVGAIGKEGATIRNITKQTSKIDVHRKEN 276
Qy 237 AGAAEKSTILSTPETSAAKSILSILMHKEAQDIKFTTEIPLKILAHNNFVGRLLGKGR 296
Db 277 AGAAEKSTILSTPETSAAKSILSILMHKEAQDIKFTTEIPLKILAHNNFVGRLLGKGR 336
Qy 297 RNKKIBQDTRKTIISPLQELTLYNPRTITVKGNVETCAKAEIEIMKKIRESYENDIA 356

Db 337 RNLKKIEQDQTKITISPLQELTLNPNERTITVKGNETCAKAEIEIMKKIRRESYENDIA 396
QY 357 SNLQAHILIPGLNALGLFPPTSGMPPPTSGPPSAMTPPYQPFQSESETVHQFIPALS 416
Db 397 SNLQAHILIPGLNALGLFPPTSGMPPPTSGPPSAMTPPSQSESETHLFPALS 456
QY 417 VCAITGKQGHITKQLSRFAGASIKITAPAEADAKVVMVLIITGPPAQAQRIYGIKE 476
Db 457 VRALISKQGHITKQLSRFAGASSKIAPVEADPAKVRVMVMIAGSPARFKAQRIYGIKE 516
QY 477 ENFVSPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVPDPDQV 536
Db 517 ENFVSPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVPDPDQV 576
QY 537 VKITGHFYACQVAQKRIQELITQVQHQQKALQSGPPQSRK 579
Db 577 VKITGHFYACQVAQKRIQELITQVQHQQKALQSGPPQSRK 619

RESULT 8

PCT-US01-08631-42951
; Sequence 42951, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 42951
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (504)...(516)
; OTHER INFORMATION: KH domain proteins family of RNA binding proteins domain
; OTHER INFORMATION: Identified by eMATRIX, accession number PF00013, p-value=1.000e-1
; OTHER INFORMATION: raw score of 5.78
; NAME/KEY: misc_feature
; LOCATION: (1)...(583)
; OTHER INFORMATION: Xaa = X or * as defined in table 2
PCT-US01-08631-42951

Query Match 92.5%; Score 2733; DB 1; Length 583;
Best Local Similarity 92.8%; Pred. No. 2.4e-180;
Matches 541; Conservative 6; Mismatches 32; Indels 4; Gaps 1;
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKYGVAFVDCPDSEWALKAIALSCK 60
Db 1 MNKPYIRNLSENAAPDLDELIGILKDAKIPVSGPFLVKYGVAFVDCPDSEWALKAIALSCK 60
QY 61 IELHGKPIEVEHSVPKRQIRKQLIRNIPPHLOWEVLDSLLVQYGVVSECEQVNTDSETA 120
Db 61 IELHGKPIEVEHSVPKRQIRKQLIRNIPPHLOWEVLDSLLVQYGVVSECEQVNTDSETA 120
QY 121 VVNVTYSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRGLQ 176
Db 121 VVNVTYSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRGLQ 180
QY 177 RGSROGSGSVSKQKPCDLPLRLVPTQFVGAIIGKEGATIRNITKTQSKIDVHRKEN 236
Db 181 RGSROGSGSVSKQKPCDLPLRLVPTQFVGAIIGKEGATIRNITKTQSKIDVHRKEN 240
QY 237 AGAAEKSTILSTPGTSAACKSILEIMHKEADIKFTTEIPLKILAHNNFVGRLLIGKEG 296
Db 237 AGAAEKSTILSTPGTSAACKSILEIMHKEADIKFTTEIPLKILAHNNFVGRLLIGKEG 296

Db 241 AGAAEKSTILSTPGTSAACKSILEIMHKEADIKFTTEIPLKILAHNNFVGRLLIGKEG 300
QY 297 RNLKKIEQDQTKITISPLQELTLNPNERTITVKGNETCAKAEIEIMKKIRRESYENDIA 356
Db 301 RNLKKIEQDQTKITISPLQELTLNPNERTITVKGNETCAKAEIEIMKKIRRESYENDIT 360
QY 357 SNLQAHILIPGLNALGLFPPTSGMPPPTSGPPSAMTPPYQPFQSESETVHQFIPALS 416
Db 361 SNLQAHILIPGLNALGLFPPTSGMPPPTSGPPSAMTPPSQSESETHLFPALS 420
QY 417 VCAITGKQGHITKQLSRFAGASIKITAPAEADAKVVMVLIITGPPAQAQRIYGIKE 476
Db 421 VRALISKQGHITKQLSRFAGASSKIAPVEADPAKVRVMVMIAGSPARFKAQRIYGIKE 480
QY 477 ENFVSPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVPDPDQV 536
Db 481 ENFVSPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVPDPDQV 540
QY 537 VKITGHFYACQVAQKRIQELITQVQHQQKALQSGPPQSRK 579
Db 541 VKITGHFYACQVAQKRIQELITQVQHQQKALQSGPPQSRK 583

RESULT 9

US-09-873-637-2
; Sequence 2, Application US/09873637
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-873-637-2

Query Match 74.1%; Score 2190; DB 5; Length 577;
Best Local Similarity 74.1%; Pred. No. 5.7e-143;
Matches 434; Conservative 62; Mismatches 74; Indels 16; Gaps 8;
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKYGVAFVDCPDSEWALKAIALSCK 60
Db 1 MNKLYIGNLSENVTPADLEKVFAEHKSISYSGQFLVKSGYAFVDCPDSEWAMKAIEFTFSK 60
QY 61 IELHGKPIEVEHSVPKRQIRKQLIRNIPPHLOWEVLDSLLVQYGVVSECEQVNTDSETA 120
Db 61 VELQKRLMEHSEHVPKQKRSKRIQIRNIPPLRWEVLDSLLAQYGVVSECEQVNTDSETA 120
QY 121 VVNVTYSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGR--GLQGRGS 179
Db 121 VVNVTYSSNEQTRQALIMKLNGHLENHALKVSYPIDPEQITQ----GPENGRRGSGRSG 176
QY 180 SRQSGP--GSVSKQKPCDLPLRLVPTQFVGAIIGKEGATIRNITKTQSKIDVHRKEN 236
Db 177 PRQGSFVAAGAPAKQOPVDIPRLVPTQYVGAIIGKEGATIRNITKTQSKIDVHRKEN 236
QY 237 AGAAEKSTILSTPGTSAACKSILEIMHKEADIKFTTEIPLKILAHNNFVGRLLIGKEG 296
Db 237 AGAAEKASIVHSTPEGSSACKMILEIMHKEADIKFTADEVPLKILAHNNFVGRLLIGKEG 296
QY 297 RNLKKIEQDQTKITISPLQELTLNPNERTITVKGNETCAKAEIEIMKKIRRESYENDIA 356
Db 297 RNLKKVEQDTEKTISSISLQDLTLNPNERTITVKGAIENCCRAEQEIMKKVREAYENDVA 356
QY 357 SNLQAHILIPGLNALGLFPPTSGMPPPTSGPPSAMTP--PPYQPEQS-ETETVHQFIP 413
Db 357 AMSLSHLIPGLNLAAGLVFPASSAVPP---PPSSVTGAAPYSFPMQAEQEMVQVFP 413

[illegible]

Query Match	66.0%	Score	1950.5	DB 1	Length	614	
Best Local Similarity	65.3%	Pred. No.	1.9e-126				
Matches	386	Conservative	81	Mismatches	95	Indels	29
							Gaps 8;
QY	1	MNKLYIGNLSENAAPS	DOLESIFDKDAKIPVSGPFLVKG	YAFVDCPD	DSWALKATEALSGK	60	
Db	17	MNKLYIGNLSPAVTAD	LRQLGDKPLAGQVLKSGYAFVDY	PDQNWAI	RAIETLSGK	76	
QY	61	IELHGKPIEVHVSVPK	RQRTKLRINPPHLOWEVLDSLLVQ	CVVESC	BOVNTDSETA	120	
Db	77	VELHGKMEVDVYSVK	KLRSKQIRINPPHLOWEVLGDLQAQ	YGTVEN	QVAVNTDRETA	136	
QY	121	VNVNYSKQARQALDK	NGFLENFTLVAYITPDEMAQQNP	LQOPGR	RGRGLQGRGSS	180	
Db	137	VNVNYYATREAKTAM	EKLSCHQFENYSFKISYIPDEEVSSP	PPQ--RAQR--	GDHSSR	192	
QY	181	ROG-SPGSVSKORPC	DLPRLVVPTQVFGAIIGKEGATIRN	TKQTQ	OSKIDVHRKENAGA	239	
Db	193	EQGHAPGGTQOARG	IDPFLRILVPTQVFGAIIGKEGUTIRN	TKTKTSQ	RSRVDIHRKNSGA	252	
QY	240	AESKSTILSTPEGTS	AACKSLEIMHKEADIDKFTETPLKLI	AHNNFVGR	LICKGEGRNL	299	
Db	253	AERPVTIHATPEGT	SEACRMILEIMQKEADETKLA	EIPLKLI	AHNGLVGR	LICKGEGRNL	312
QY	300	KKIEQDPTDKITIS	PLQELTYLNPERTITYKGVN	YETCAK	APEEIMKKIR	ESYENDIASMN	359
Db	313	KKIEHETGTRKITS	LODLSITYNPERTITVKGTV	EACASAEI	ETMKKLR	AFENDMLAVN	372

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Qy 360 LQAHLIPGLNLNALGLF-----PETS--GMPPPT-----SGPPSAMTP-----p 396
Db 373 QOANLEIPLGLNLSALGIFSTGLSVLSPAGPRGAPPAAPIYHPFTTHSGYTSSLYPHHQFGP 432
Qy 397 YPOEQE-SETETVHOFTPALSYGAIIICKQOHIKQLSRFAGASIKITAPAEADPAKVRMVI 455
Db 433 FPHHHSYPEQEIVNLFIPTQAVGAILIGKGAHIKQLARFAGASIKITAPAEGPDSERMWI 492
Qy 456 ITGPPEAQFRAQGRIRYKGRIKEENFVSPEEKVEKLEAHIRVPSPAAGRIVGKGGKTVELQN 515
Db 493 ITGPPEAQFRAQGRIFGCKLEEENFNPEKEEVKLEAHIRVPSSTAAGRIVGKGGKTVELQN 552
Qy 516 LSSAEVVPRDQTDPDENQDVVKITGHFYACQVAQRKIQBIILTVQVKOHQQQ 566
Db 553 LTSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAKRKIREIVQOVKQEQK 603

RESULT 11
US-09-764-864-1116
; Sequence 1116, Application US/09764864
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1116
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (533)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino ac
US-09-764-864-1116
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[illegible]

QY 397 YPOFEQ-SETETVHQIPALSVGAILGKQCOHOKIOLSRFAGASIKIAPAEAPDAKVRMVI 455
Db 439 FPHHSYPOEIVNLFPTQAVGAILGKGAHIKQLARFAGASIKIAPAEAPDAKVRMVI 498
QY 456 ITGPPPEAKQAQRIYKGIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQN 515
Db 499 ITGPPPEAKQAQRIYKGIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQN 558
QY 516 LSSAEVVPDPTDNDQVVKITGHFYACQVAQRKIQEILTVQVQKHOQOO 566
Db 559 LTSAEVVPDPTDNDQVVKITGHFYACQVAQRKIQEILTVQVQKHOQOO 609

RESULT 12
PCT-US01-08631-37154
; Sequence 37154, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 37154
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (43)..(62)
; OTHER INFORMATION: Eukaryotic RNA-binding region RNP-1 proteins domain
; OTHER INFORMATION: identified by EMATRIX, accession number BL00030A, p-value=4.938e-
; OTHER INFORMATION: 12, raw score of 14.39
; NAME/KEY: DOMAIN
; LOCATION: (235)..(558)
; OTHER INFORMATION: KH domain identified by Pfam, accession name KH-domain, E-
; OTHER INFORMATION: value=1.8e-51, Pfam score of 184.4
PCT-US01-08631-37154

Query Match 63.2%; Score 1868; DB 1; Length 594;
Best Local Similarity 64.8%; Pred. No. 8.8e-121;
Matches 368; Conservative 78; Mismatches 96; Indels 26; Gaps 6;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPPLVKTGVAFYDCPDSEWALKAEALSGK 60
Db 40 MNKLYIGNLSPAVTADLRQLFGDRKLPLAGQVLLKSGYAFVDPQNWAIKRAIETLSGK 99
QY 61 IELHGKPIEVHSPKQRTRKQIRNIPHLQWELDSLIVQYGVVSCSEQVNTDSETA 120
Db 100 VELHGKIMEVDYISVSKRLSKQIRNIPHLQWELDGLLAQYGVENVQVNTDTEA 159
QY 121 VNVVTYSSKDOARQALDKLNGFLENFTLKVAYIPDEMAAQNPLOQPRGRRLGORGSS 180
Db 160 VNVVTATREEAKIAMEKLSGHOFENYSEKISVIPDEEVSSPPQ--RAQR--GDHSSR 215
QY 181 RQG-SFGSVSKQPCDLPURLLVPTQFVGAIIGKEGATRNITKQTSKIDVHRKNAGA 239
Db 216 EQGHAPGTSQARQIDFPLRLVPTQFVGAIIGKEGATRNITKQTSKIDVHRKNAGA 275
QY 240 AKSITLTPSECTSACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLGKGRNL 299
Db 276 AEPVTHATPEGTSEACRMILSIMEQADETKLAEIPLKILAHNNFVGRLLGKGRNL 335
QY 300 KKIEQDQDTKITISPLQELTYNPRTITVKGNETCAKAEIEMKKIRSYENDIASMN 359
Db 336 KKIEHETGKITISSLQDLSIYNPRTITVKGNETCAKAEIEMKKIRSYENDIASMN 395

QY 360 LQAHILPGLNMLNALGLFPPTSGMPPTSGPPSAMTPPYPOFEQ-SETETVHQIPALSVG 418
Db 396 THS-----GTF-----SSLYPHHQFGFPFHHHSYPOEIVNLFPTQAVG 435
QY 419 AITGKQGOHIKOLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAKQAQRIYKGIKEEN 478
Db 436 AITGKGAHIKQLARFAGASIKIAPAEAPDAKVRMVIITGPPPEAKQAQRIYKGIKEEN 495
QY 479 FVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVPDPTDNDQVVK 538
Db 496 FPNPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVPDPTDNDQVVK 555
QY 539 ITGHFYACQVAQRKIQEILTVQVQKHOQOO 566
Db 556 IGHFFASQTAQRKIREIVQVQKHOQOO 583

RESULT 13
US-09-760-466-1096
; Sequence 1096, Application US/09760466
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT259
; CURRENT APPLICATION NUMBER: US/09/760,466
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1813
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1096
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (318)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (330)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-760-466-1096

Query Match 51.2%; Score 1512; DB 5; Length 334;
Best Local Similarity 96.5%; Pred. No. 1.2e-96;
Matches 300; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 228 KIDVHRKENAGAAEKSTITILSTPEGTSAAKSSILEIMHKEAQDIKFTTEIPLKILAHNNF 287
Db 24 RIDVHRKENAGAAEKSTITILSTPEGTSAAKSSILEIMHKEAQDIKFTTEIPLKILAHNNF 83
QY 288 VGRLLCKEGRNLAKIEQDQTKITISPLQELTYNPRTITVKGNETCAKAEIEMKKI 347
Db 84 VGRLLCKEGRNLAKIEQDQTKITISPLQELTYNPRTITVKGNETCAKAEIEMKKI 143
QY 348 RESYENDIASMNLOAHILPGLNMLNALGLFPPTSGMPPTSGPPSAMTPPYPOFEQSETET 407
Db 144 RESYENDIASMNLOAHILPGLNMLNALGLFPPTSGMPPTSGPPSAMTPPYPOFEQSETET 203
QY 408 VHQFIPALSVGAILGKQCOHOKIOLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAKQA 467
Db 204 VHLFIPALSVGAILGKQCOHOKIOLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAKQA 263
QY 468 GRVYGIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVPDQ 527
Db 264 GRVYGIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVPDQ 323
QY 528 TPDNDQVVK 538
Db 324 HLMRMDXVVK 334

RESULT 14

US-09-764-864-1114

; Sequence 1114, Application US/09764864
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1114
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1114

Query Match 32.1%; Score 949; DB 5; Length 261;
Best Local Similarity 74.5%; Pred. No. 4.9e-58;
Matches 193; Conservative 26; Mismatches 32; Indels 8; Gaps 5;

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Qy 324 ERTIVKGVETCAKAEIEIMKKIRESYENDIASNMQAHLIPGLNLNALGLFPPTSGMP 383
Db 8 ERTIVKGAIECCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAAGLFPASSAV 67
Qy 384 PPTSGPPSMT--PPYPOFEQS-ETETVHQFIPALSVGAIIKGQGHKQLSRFAGASIK 440
Db 68 PP---PPSSVTGAAPYSSFMQAPQEQEMVQVFIPAQAAGVGAIIKGKQGHKQLSRFASAIK 124
Qy 441 IAPAEAPDAKVRMVIITGPPPEAQFKAQGRIRYCKIKEENFVSPKEEVKLEAHIRVPSFAAG 500
Db 125 IAPETPSKVRMVIITGPPPEAQFKAQGRIRYCKIKEENFVSPKEEVKLEAHIRVPSAAG 184
Qy 501 RVIGKGTVNELQNLSSAEVVVPRDQTPDENDQVVVKITGHFYACQVAQRKIQEIITQV 560
Db 185 RVIGKGTVNELQNLTAEEVVVPRDQTPDENDQVVVKITGHFYASQMAQRKIRDLAQV 244
Qy 561 KOHOOAKALQSGPPQSRRK 579
Db 245 KO-QHKG-QSNOQAARRK 261

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RESULT 15

US-09-764-864-1532
; Sequence 1532, Application US/09764864
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1532
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (134)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1532

Query Match 31.1%; Score 919; DB 5; Length 250;
Best Local Similarity 73.3%; Pred. No. 5.3e-56;
Matches 187; Conservative 26; Mismatches 34; Indels 8; Gaps 5;

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Qy 328 TVKGNVETCAKAEIEIMKKIRESYENDIASNMQAHLIPGLNLNALGLFPPTSGMPPTS 387
Db 1 TVKGAIECCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAAGLFPASSAVPP-- 58
Qy 388 GPPSMT--PPYPOFEQS-ETETVHQFIPALSVGAIIKGQGHKQLSRFAGASIKIAPA 444
Db 59 -PPSSVTGAAPYSSFMQAPQEQEMVQVFIPAQAAGVGAIIKGKQGHKQLSRFASIKIAPP 117
Qy 445 EAPDAKVRMVIITGPPPEAQFKAQGRIRYCKIKEENFVSPKEEVKLEAHIRVPSFAAGRVIG 504
Db 118 ETPDSKVRMVIITGPPPEAQFKAQGRIRYCKIKEENFVSPKEEVKLEAHIRVPSAAGRVIG 177
Qy 505 KGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKITGHFYACQVAQRKIQEIITQVQKHQ 564
Db 178 KGGKTVNELQNLTAEEVVVPRDQTPDENDQVVVKITGHFYASQMAQRKIRDLAQVKQ-Q 236
Qy 565 OOKALQSGPPQSRRK 579
Db 237 HOKG-QSNOQAARRK 250

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Search completed: September 29, 2001, 14:05:40
Job time: 723 sec


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Search information block:
Query: US-09-466-396A-176
Query length: 579
Database: Pending_Patents_NA_Main:*
Database sequences: 14155048
Database length: -1201529497
Search time (sec): 2118.450000
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alignment_scores:
  Quality: 2956.00      Length: 579
  Ratio: 5.105          Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-466-396A-176 x US-09-061-709-4      ..

Align seg 1/1 to: US-09-061-709-4 from: 1 to: 4159

1 MetAsnLysLeuTyrIleGlyAsnLeuSerGluAsnAlaAlaProSerAs 17
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|||||
|||||
|||||
251 ATGACAAACTGTATATCGGAAACCTCAGCGAGAACGCCGCCCTCGGA 300
|||||
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|||||
|||||
17 pIeuGluSerIlePheLysAspAlaLysIleProValserGlyProPheL 34
|||||
|||||
|||||
|||||
301 CCTAGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTCGGGACCTTCC 350
|||||
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|||||
|||||
34 euValIysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
|||||
|||||
|||||
|||||
351 TCGTGAAGACTGGCTACGGCTTCGTGGACTCCCGGACGAGAGCTGGGCC 400
|||||
|||||
|||||
|||||
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
|||||
|||||
|||||
|||||
401 CTCAGGCCATCGAGGGCGCTTTCAGGTAAATAGAAGTGCACGGGAACCC 450
|||||
|||||
|||||
|||||
67 otIleGluValGluHisSerValProLysArgGlnArgIleargLysLeuG 84
|||||
|||||
|||||
|||||
451 CATAGAAGTTGAGCACTCGGTCGCCAAAAGCAAGGATTCGGAAACATTC 500
|||||
|||||
|||||
|||||
84 InIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
|||||
|||||
|||||
|||||
501 AGATACGAAATATCCGCCCTCATTTACAGTGGGAGGTCTCGGATAGTTTA 550
|||||
|||||
|||||
|||||
101 LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe 117
|||||
|||||
|||||
|||||
551 CTAGTCCAGTATGGAGTGGTGAGAGCTGTGAGCAAGTGAACACTGACTC 600
|||||
|||||
|||||
|||||
117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG 134
|||||
|||||
|||||
|||||
601 GCAAACTCGAGTTGTAATCTGAACCTATTCACGTAAAGCAACCAAGCTAGC 650
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134 InAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLys 150
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651 AAGCACATAGACAACATGAATGATTTACGTTAGACAATTTACCTTGAAA 700
|||||
151 ValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnG1 167
|||||
701 GTAGCCTATATCCCTGATGAATGCCGCCACAGCAAAACCCCTTGACGCA 750
|||||
167 nProArgGlyArgGlyLeuGlyGlnArgGlySerArgGlnGlyS 184
|||||
751 GCCCGAGGTCCCGGGGCTTGGCGCAGAGGGGCTCCTCAAGCGAGGGGT 800
|||||
184 exProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu 200
|||||
801 CTCAGGATCCCTATCCAAGCAGAAACCATGATTTGCCCTCTGCCCTG 850
|||||
201 LeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaTh 217
|||||
851 CTGGTTCCCAACCAATTTGTTGGAGCCATCATAGGAAAGAGGTGCCAC 900
|||||
217 rIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgL 234
|||||
901 CATTCGGAAACATCACCAACAGACCCAGTCTAATAATCGATGTCACCGTA 950
|||||
234 ysGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrPro 250
|||||
951 AAGAAATGCGGGGCTGCTGAGAAGTCGATTACTCTCTCTACTCCT 1000
|||||
251 GluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLysG1 267
|||||
1001 GAAGGCACCTCTGCGGCTGTGAAGTCTATTCTGGAGATTATGCATAAGGA 1050
|||||
267 uAlaGlnAspIleLysPheThrGluGluIleProLeuLysIleLeuAlaH 284
|||||
1051 AGCTCAGAGTATAAATTCACAGAGAGATCCCTTGAGATTTTAGCTC 1100
|||||
284 IsAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLys 300
|||||
1101 ATAATAACTTTCTGGAGCTCTATTGTTAAAGAGAAAGAAATCTTAAA 1150
|||||
301 LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnG1 317
|||||
1151 AAAATTGAGCAAGACAGACACTAAATACGATATCTCCATTGCAGGA 1200
|||||
317 uLeuThrLeuTyrAsnProGluArgThrIleThrValLysGlyAsnValG 334
|||||
1201 ATTGACGCTGTATATCCAGAACGCACTATTACAGTTAAAGCAATGTTG 1250
|||||
334 luThrCysAlaLysAlaGluGluGluIleMetLysLysIleArgGluSer 350
|||||
1251 AGACATGTCCCAAAGCTGAGGAGGAGATCATGAAGAAATCAGGGAGTCT 1300
|||||
351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProG1 367
|||||
1301 TATGAATGATGATTGCTTCTATGAATCTTCAAGCACATTTAATTCCTGG 1350
|||||
367 yLeuAsnLeuAsnAlaLeuGlyLeuPheProProThrSerGlyMetProp 384
|||||
1351 ATTAATCTGAACGCTTGGGTCTGTTCCCAACCACTTCCAGGGATGCCAC 1400
|||||
384 roProThrSerGlyProProSerAlaMetThrProProTyrProGlnPhe 400
|||||
1401 CTCGCCACCTAGGGGCCCTTTCAGGCATGACTCTCCCTACCCGAGTTT 1450
|||||
401 GluGlnSerGluThrGluThrValHisGlnPheIleProAlaLeuSerVa 417
|||||
1451 GAGCAATCAGAAACGAGACTGTTCTATCAGTTTATCCAGCTCTATCAGT 1500
|||||
417 lGlyAlaIleIleGlyLysGlnGlnHisIleLysGlnLeuSerArgp 434
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1501 CGGTGCCATCATCGCAAGCAGGGGCCAGCATCAAGCAGCTTCTCTCGCT 1550
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434 heAlaGlyAlaSerIleLysIleAlaProAlaGluAlaProAspAlaLys 450
|||||
1551 TTGCTGGAGCTTCAATTAAGATTGCTCAGCGGAAAGCACCAGATGCTAAA 1600
|||||
451 ValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaG1 467
|||||
1601 GTGAGGATGGTGATTATCACTGGACCACCAGAGGCTCAGTTCAAGGCTCA 1650
|||||
467 nGlyArgIleTyrGlyLysIleLysGluGluAsnPheValSerProLysG 484
|||||
1651 CGCAACAATTTATGAAAAATTAAGAAAGAAACCTTTGTTAGTCTCTAAAG 1700
|||||
484 luGluValLysLeuGluAlaHisIleArgValProSerPheAlaAlaGly 500
|||||
1701 AAGAGGTGAAACTTCAAGCTCATATCAGAGTCCATCTCTTCTGCTGGC 1750
|||||
501 ArgValIleGlyLysGlyLysThrValAsnGluLeuGlnAsnLeuSe 517
|||||
1751 AGAGTTATTGGAAAAAGGAGGCAAAACGGTGAATGAATTCAGAAATTTGTC 1800
|||||
517 rSerAlaGluValValValProArgAspGlnThrProAspGluAsnAspG 534
|||||
1801 AAGTCCAGAAGTTGTTGCCCTCGTGACCAGACCTGATGAGAATGACC 1850
|||||
534 InValValLysIleThrGlyHisPheTyrAlaCysGlnValAlaGln 550
|||||
1851 AAGTGGTTGTCAAAATAACTGGTCACTTCTATGCTTGCCAGGTTGCCCAG 1900
|||||
551 ArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnGlnly 567
|||||
1901 AGAAAAATTCAGGAAATTTCTGACTCAGGTAAAGCAGCACCAACACAGAA 1950
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567 sAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
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1951 GCCTCTGCAAGAGTGACCACTCACTCAAGACGGAAG 1987
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seq_documentation_block:

- : Sequence 4, Application US/09270437A
- : GENERAL INFORMATION:
- : APPLICANT: Chen, Yao-Tseng
- : APPLICANT: Gure, Ali
- : APPLICANT: Tsang, Solam
- : APPLICANT: Stockert, Elisabeth
- : APPLICANT: Jager, Elke
- : APPLICANT: Knuth, Alexander
- : APPLICANT: Old, Lloyd J.
- : TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Ant
- : TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
- : FILE REFERENCE: LUD 5538.1 PCT
- : CURRENT APPLICATION NUMBER: US/09/270,437A
- : CURRENT FILING DATE: 1999-03-16
- : NUMBER OF SEQ ID NOS: 8
- : SEQ ID NO 4
- : LENGTH: 4159
- : TYPE: DNA
- : ORGANISM: Homo sapiens
- : FEATURE:

US-09-270-437-4

alignment_scores:

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Ratio:	5.105 <td>Gaps:</td> <td>0</td>	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-466-396A-176 x US-09-270-437-4

Align seg 1/1 to: US-09-270-437-4 from: 1 to: 4159

1 MetAsnLysLeuTyrIleGlyAsnLeuSerGluAsnAlaAlaProSerAs 17

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251 ATGACAAACTGTATATCGGAACCTCAGGAGAACGCCGCCCTCGGA 300
17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
|||||
301 CCTAGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTCGGGACCTTCC 350
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
|||||
351 TGTGTAAGACTGGCTACGGGTTCGTGGACTGCCCGGACGAGAGCTGGCC 400
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
|||||
401 CTCAGGCCATCAGCGGCTTTCAGGTAAATAGAACTGCACGGGAACC 450
67 olleGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
|||||
451 CATAGAAGTTGAGCACTCGGTCCCAAAAGCAAGGATTCGGAACCTC 500
84 lnIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
|||||
501 AGATACGAATATCCCGCCCTCATTTACAGTGGAGGTGCTGGATGTTTA 550
101 LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe 117
|||||
551 CTAGTCCAGTATCGAGTGTGGAGACTGTGAGCAAGTGAACACTGACTC 600
117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG 134
|||||
601 GGAACCTGCAGTTGTAATGTAACTTATCCACTAAGGACCAAGCTAGAC 650
134 lnAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLys 150
|||||
651 AAGCACTAGACAAACTGAATGGATTTTCAGTTAGAGAAATTTACCTTGA 700
151 ValAlaTyrIleProAspGluMetAlaAlaGlnGluAsnProLeuGlnG 167
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701 GTAGCTTATATCCTGATGAATTTGGCCGCCACGAAACCCCTTGCAGCA 750
167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerArgGlnGlyS 184
|||||
751 GCCCCGAGGTGCGCGGGGCTTGGCAGAGGGGCTCCTCAAGCGAGGGT 800
184 erProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu 200
|||||
801 CTCAGGATCCGTATCCCAAGCAGAAACCATGTGATTTGCCCTCTCGCGCTG 850
201 LeuValProThrGlnPheValGlyAlaIleGlyLysGluGlyAlaTh 217
|||||
851 CTGGTCCCACCCCAATTTGTTGAGGCATCATAGGAAAGAGGTGCCAC 900
217 rIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgL 234
|||||
901 CATTCGGAACATCACCAACAGACCCAGCTCTAAATCGATGTCCACCGTA 950
234 yGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrPro 250
|||||
951 AAGAAATCGGGGGTGTCTGAGAAGTCGATTACTATCCTCTCTACTCCT 1000
251 GluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMethLysGly 267
|||||
1001 GAAGGACCTCTCGGGCTTGTAGTCTTATTCGTGGAGATTATGCATAGGA 1050
267 uAlaGlnAspIleLysPheThrGluGluIleProLeuLysIleLeuAlaH 284
|||||
1051 AGCTCAAGATATAAATTCACAGAAGAGATCCCTTGAAGATTTAGCTC 1100
284 isAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLys 300
|||||
1101 ATAATACTTTTGTGGACGTCATTATTGGTAAAGAAAGGAGAAATCTTAA 1150
301 LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnG 317
|||||
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1151 AAATTTGAGCAACACACAGACACTAAATACAGATATCTCCATTGCAGGA 1200
317 uLeuThrLeuTyrAsnProGluArgThrIleThrValLysGlyAsnValG 334
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1201 ATTGACGCTGTATAATCCAGAACGCACTATTACAGTTAAAGCAATGTG 1250
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351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProG 367
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1301 TATGAANAATGATATTGCTTCTATGAATCTTCAAGCACATTTAATTCCTGG 1350
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; Sequence 175, Application US/09466396A
; GENERAL INFORMATION:
; APPLICANT: Wang, TongLong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND

;; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
;; FILE REFERENCE: 210121.455C4
;; CURRENT APPLICATION NUMBER: US/09/466,396A
;; CURRENT FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 175
;; LENGTH: 4181

;; TYPE: DNA
;; ORGANISM: Homo sapiens

;; FEATURE:

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;; OTHER INFORMATION: n=A,T,C or G

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301 CTAGAAAGTATCTTCAAGAGCGCCCAAGATCCCGGTGTCGGAGCCCTTCC 350
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34 euValLysThrGlyTyrAlaPheValAspCysProAspLysSerTrpAla 50
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; Sequence 175, Application US/09542615A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun

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; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
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; SOFTWARE: FastSeq for Windows Version 3.0
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; ORGANISM: Homo sapiens
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301 CCTAGAAAGTATCTTCAAGCAGCCCAAGATCCCGGTGTCGGGACCTTCC 350
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
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51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
401 CTCAGGCCATCGAGCGCTTTCAGGTAAATAGAACTGCACGGGAACCC 450
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: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C10
: CURRENT APPLICATION NUMBER: US/09/630,940A
: CURRENT FILING DATE: 2000-08-02
: SOFTWARE: FastSEQ for Windows Version 3.0
: SEQ ID NO 175
: LENGTH: 4181
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (3347)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (3502)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (3506)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (3520)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (3538)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (3549)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (3646)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (3940)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (3968)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (3974)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (4036)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (4056)
: OTHER INFORMATION: n=A,T,C or G
: NAME/KEY: unsure
: LOCATION: (4062)
: OTHER INFORMATION: n=A,T,C or G

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; NAME/KEY: unsure
; LOCATION: (4080)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (4088)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (4115)
; OTHER INFORMATION: n=A,T,C or G
US-09-466-396A-176

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alignment_scores:
  Quality: 2956.00      Length: 579
  Ratio: 5.105          Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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alignment_block:

US-09-466-396A-176 x US-09-630-940A-175

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251 ATGACAAACTGTATATCGAAGACCTCAGGAGACGCCGCCCTCGGA 300
17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
301 CCTAGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTCGGGACCTTC 350
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
351 TGGTCAAGACTGGCTACGCCCTTCGTGACTGCCCGGACGAGCTGGGCC 400
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
401 CTCAGGCCATCGAGGCGCTTTCAGGTAAATAGAACTGCACGGGAACC 450
67 oLeGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
451 CATAGAAAGTTGAGCACTCGGTCCCAAAAGCAAAAGGATTCGGAAACT 500
84 nIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
501 AGATACCAAAATATCCGCCCTCATTTACAGTGGAGGTGCTGGATAGTTA 550
101 LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe 117
551 CTAGTCCAGTATGGAGTGGGAGAGCTGTGACCAAGTGAACACTGACTC 600
117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG 134
601 GGAACCTGCAGTTGTAATGTAACTTATCCAGTAAGSACCAAGCTAGAC 650
134 nAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLys 150
651 AAGCACTAGACAAACTGAATCGATTTCAGTTAGAGAAATTCACCTTGAA 700
151 ValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnG 167
701 GTAGCCTATATCCCTGATGAAATGGCCGCCAGCAAAACCCCTTGCAGCA 750
167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerSerArgGlnLys 184
751 GCCCGAGGTGCGCGGGGCTTGGGAGAGGGGCTCCTCAAGGACAGGGGT 800
184 erProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu 200
801 CTCAGGATCCGATCCAAAGCAGCAAAACCATGTGATTTGCCCTCTCGCCTG 850
201 LeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaTh 217
851 CTGGTTCACCCCAANTTTGTTGGAGCCCATCATAGGAAAGAGGTGCCAC 900

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217 rIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgL 234
901 CATTCGGGAACATCACCAACAGACCCAGTCTAAAATCGATGTCACCGTA 950
234 ySGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrPro 250
951 AAGAAAATCGGGGCTGCTGAGAAAGTCGATTACTATCTCTCTACTCCT 1000
251 GluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMethHisLysG 267
1001 GAAGGCACCTCTCGGGCTTGTAGCTTATCTGGAGATTATGCATAAGGA 1050
267 uAlaGlnAspIleLysPheThrGluGluIleProLeuLysIleLeuAlaH 284
1051 AGCTCAAGATATAAAATTCACAGAAGAGATCCCTTCAAGATTTTAGCTC 1100
284 iAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLys 300
1101 ATAATAACTTTTGTGGACGCTTATTTGGTAAAGAAAGGAATAATCTTAA 1150
301 LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnG 317
1151 ARAATTGAGCAAGACACAGACACTAAATCACGATATCTCCATTGCAGGA 1200
317 uLeuThrLeuTyrAsnProGluArgThrIleThrValLysGlyAsnValG 334
1201 ATTCACGCTGTATAATCCAGAACGCACTATTACAGTTAAAGGCAATGTTG 1250
334 luThrCysAlaLysAlaGluGluGluIleMetLysLysIleArgGluSer 350
1251 AGACATGTGCCAAAGCTGAGGAGGAGATCATGAAGAAATCAGGGAGTCT 1300
351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProG 367
1301 TATGAAATGATATTGCTTCTATGAATCTTCAACACATTTAATTCCTGG 1350
367 yLeuAsnLeuAsnAlaLeuGlyLeuPheProProThrSerGlyMetProp 384
1351 ATTAATCTGAACCCCTTGGGCTCTGTTCCCAACCCACTTCAGGGATGCCAC 1400
384 rProThrSerGlyProProSerAlaMetThrProProTyrProGlnPhe 400
1401 CTCACCTCAGGGCCCCCTTCAGCCATGACTCTCTCCCTACCCGCACTT 1450
401 GluGlnSerGluThrGluThrValHisGlnPheIleProAlaLeuSerVa 417
1451 GAGCAATCAGAAACGAGAGACTGTTTCATCAGTTTATCCAGCTCTATCAGT 1500
417 lGlyAlaIleIleGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgp 434
1501 CGGTGCCATCATCGCAAGCAGGCGCCAGCACATCAAGCAGCTTCTCGCT 1550
434 heAlaGlyAlaSerIleLysIleAlaProAlaGluAlaProAspAlaLys 450
1551 TTGCTGGAGCTTCAATTAAGATTGCTCCAGCGAAGCACCAGATGCTAAA 1600
451 ValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaG 467
1601 GTGAGGATGGTATTATCCTGGACCCAGGAGGCTCAGTTTCAAGGCTCA 1650
467 nGlyArgIleTyrGlyLysIleLysGluGluAsnPheValSerProLysG 484
1651 GGGAGAAATTTATGAAAAATTAAGAAAGAAACTTTCTTAGTCTCTAAAG 1700
484 luGluValLysLeuGluAlaHisIleArgValProSerPheAlaAlaGly 500
1701 AAGAGGTGAAACTTGAAGCTCATATCAGAGTGCCATCCTTTGCTGCTGGC 1750
501 ArgValIleGlyLysGlyLysThrValAsnGluLeuGlnAsnLeuSe 517
1751 AGGTTATTGAAAAGGAGGCAAAACGGTGAATGAACCTTCAAGATTTGTC 1800

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517 rSerAlaGluValValProArgAspGlnThrProAspGluAsnAspG 534
|||||
1801 AAGTCGAGAGTGTGTTCCTCGTCACGAGACACCTGATGAGATGACC 1850
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534 InValValValLysIleThrGlyHisPheTyrAlaCysGlnValAlaGln 550
|||||
1851 AAGTGGTTGTCAAATAACTGGTCACTTCTATGCTTGCAGGTGCCCCAG 1900
|||||
551 ArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnGlnly 567
|||||
1901 AGAAAAATTCAGCAAAATTCGACTCAGGTAAAGCAGCAGCAACACAGAA 1950
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seq_documentation_block:
; Sequence 175, Application US/09630940B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3347)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (3502)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
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; NAME/KEY: unsure
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; OTHER INFORMATION: n=A,T,C or G
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alignment_scores:
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    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-466-396A-176 x US-09-630-940B-175

Align seg 1/1 to: US-09-630-940B-175 from: 1 to: 4181

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17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
|||||
301 CCTAGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTCGGACCTTCC 350
|||||
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
|||||
351 TGGTGAAGACTGGCTGACGCTTGGGACTGCCGACGAGAGCTGGGCC 400
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51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
|||||
401 CTCAGGCCATCGAGCGCTTTTCAGGTAAATAGAACTGCACGGAAACC 450
|||||
67 OtIleGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
|||||
451 CATAGAAGTTGAGCACTCGTCCCAAAAGGCAAGGATTCGGAACCTTC 500
|||||
84 InIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
|||||
501 AGATACGAATATATCCGCTCATTTACAGTGGGAGGTGCTGGATAGTTTA 550
|||||
101 LeuValGlnTyrGlyValValGluSerCysGlnGlnValAsnThrAspSe 117
|||||
551 CTAGTCCAGTATGGAGTGGTGAGAGCTGTGAGCAAGTGAACACTGACTC 600
|||||
117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG 134
|||||
601 GGAAACTGCAGTTGTAATGTAACTATTTCCAGTAAGGACCAAGCTAGAC 650
|||||
134 InAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPhethrLeuLys 150
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651 AAGCACTAGACAAACTGAATGGATTTCAGTTAGAGAAATTTACCTTGAAA 700
|||||
151 ValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnG 167
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167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGlyS 184
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801 CTCAGGATCCGTATCCAAAGCAGAAACCATGTGATTTGCGCTCTGCGCCTG 850
|||||
201 LeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaIth 217
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851 CTGGTTCCCAACCAATTTGTTGGAGCCATCATAGGAAAGAGGTGCCAC 900
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217 rIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgL 234
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901 CATTCGGAACATCACCAACAGACCCAGTCTAAATCGATGCCACCGTA 950
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234 ysGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrPro 250
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951 AAGAAATATCGGGGCTGCTGAGAAGTCGATTACTATCCCTCTCTACTCCT 1000
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351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProGI 367
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1301 TATGAAATGATATTGCTTCTATCAATCTTCAAGCACATTTAATTCCTGG 1350
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367 yLeuAsnLeuAsnAlaLeuGlyLeuPheProProThrSerGlyMetProp 384
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1351 ATTAATCTGAACCCCTTGGGTCTGTTCACCCACCTTCAGGGATGCCAC 1400
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384 roProThrSerGlyProProSerAlaMetThrProProTyrProGlnPhe 400
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1401 CTCACCTCAGGCGCCCTTCAGCCATGACTCTCCCTACCCGCACTTT 1450
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401 GluGlnSerGluThrGluThrValHisGlnPheIleProAlaLeuSerVa 417
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417 lGlyAlaIleIleGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgp 434
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451 ValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaGI 467
|||||
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467 nGlyArgIleTyrclyLysIleLysGluAsnPheValSerProLysG 484
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seq_name: /cgn2_6/ptodata/2/pna/US096c_COMB.seq:us-09-643-597-175

seq_documentation_block:

; Sequence 175, Application US/09643597

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 175

; LENGTH: 4181

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (3347)

; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

; LOCATION: (3502)

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US-09-643-597-175

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Ratio: 5.105          Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

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Align seg 1/1 to: US-09-643-597-175 from: 1 to: 4181

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17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
301 CCTAGAAAGTATCTTCAGGACGCCCAAGATCCCGGTGTCGGGACCTTCC 350
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
351 TGGTGAAGACTGGCTACCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTG 400
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
401 CTCACGCCCATCGAGCGCTTTCAGGTAATAATAGAACTGCACGGGAAACC 450
67 oileGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
451 CATAGAAAGTTGAGCACTCGGTCCCAAAAGGCAAGAGATTCGGAACCTTC 500
84 InLeuArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
501 AGATACGAAATATCCCGCTCATTTACAGTGGGAGGTGCTGGATAGTTTA 550
101 LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe 117
551 CTAGTCCAGTATGGAGTGGTGGAGAGCTGTGAGCAAGTGAACACTGACTC 600
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151 ValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnG 167
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167 nProArgGlyArgGlyLeuGlyGlnArgGlySerSerArgGlnGlyS 184
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; Sequence 175, Application US/09662786
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C12
; CURRENT APPLICATION NUMBER: US/09/662,786
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 4181
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; Sequence 175, Application US/09685696

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C13

; CURRENT APPLICATION NUMBER: US/09/685,696

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 175

; LENGTH: 4181

; TYPE: DNA

; ORGANISM: Homo sapiens

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alignment_block:
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Align seg 1/1 to: US-09-685-696-175 from: 1 to: 4181

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|||||
251 ATGAACAAACGTATATCGGAACCTCAGGAGACGCCGCCCTCGGA 300

17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
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1451 GAGCAATCAGAAACGAGACTCTTCATCAGTTATCCAGCTCTATCACT 1500
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417 IglyAlaIleIleGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgP 434
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1501 CGGTGCCATCATCGGCAAGCAGGGCCAGCACATCAAGCAGCTTCTCGCT 1550
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434 heAlaGlyAlaSerIleLysIleAlaProAlaGluAlaProAspAlaLys 450
|||||
1551 TTGCTGGAGCTTCATTAAGATTGCTCAGCGGAAGCACCAGATCTAAA 1600
|||||
451 ValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaG1 467
|||||
1601 GTGAGGATGGTGAATTATCACTGGACACAGAGGCTCAAGGCTCA 1650
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467 nGlyArgIleThrGlyLysIleLysGluGluAsnPheValSerProLysG 484
|||||
1651 GGGAGAATTTATGGAAATTAAGAAATTAAGAAATTTGTTAGTCTCTAAG 1700
|||||
484 luGluValLysLeuGluAlaHisIleArgValProSerPheAlaAlaGly 500
|||||
1701 AAGAGTGAAACTTCAAGCTCATATCAGAGTCCATCTTTGCTGCTGGC 1750
|||||
501 ArgValIleGlyLysGlyLysThrValAsnGluLeuGlnAsnLeuSe 517
|||||
1751 AGAGTTATTGGAAAAGGAGGCAAAACGGTGAATGAATTCAGAAATTTGTC 1800
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517 rSerAlaGluValValAlaProArgAspGlnThrProAspGluAsnAspG 534
|||||
1801 AGTCGAGAAATTTGTTCCCTCGTGACGACGACCTGATGGAATGACC 1850
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534 InValValLysIleThrGlyHisPheTyrAlaCysGlnValAlaGln 550
|||||
1851 AACTGTTCTCAAAATAACTGCTCACTTCTATGCTTGCAGGTTGCCACG 1900
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551 ArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnIly 567
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1901 AGAAAAATTCAGGAAATTTCTGACTCAGGTAAGCAGCACCACACAGAA 1950
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567 saAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
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1951 GGCTCTGCAAGTGGACCACTCACTCAAGACGGGAG 1987
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seq_documentation_block:

; Sequence 175, Application US/09735705

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C14

; CURRENT APPLICATION NUMBER: US/09/735,705

; CURRENT FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 419

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 175

; LENGTH: 4181

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (3347)

; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

; LOCATION: (3502)

; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

; LOCATION: (3506)

; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

; LOCATION: (3520)

; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

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; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

; LOCATION: (3549)

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; NAME/KEY: unsure

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; NAME/KEY: unsure

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; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

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; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

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; NAME/KEY: unsure

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; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

; LOCATION: (4088)

; OTHER INFORMATION: n=A,T,C or G

; NAME/KEY: unsure

; LOCATION: (4115)

; OTHER INFORMATION: n=A,T,C or G

; US-09-735-705-175

alignment_scores:

Quality: 2956.00 Length: 579

Ratio: 5.105 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-466-396A-176 x US-09-735-705-175

Align seg 1/1 to: US-09-735-705-175 from: 1 to: 4181

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17	pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL	34
301	CCTAGAAAGTATCTTCAGGACGCCAAGATCCCGGTGTCGGGACCTTC	350
34	euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla	50
351	TGGTGAAGACTGGCTACGCGCTTCTGGACTCCCGGACGAGAGCTGGCC	400
51	LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr	67
401	CTCAAGGCCATCGAGGCGCTTTCAGGTAAATAGAATCTCACGGGAAC	450
67	oileGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG	84
451	CATAGAAGTTGAGACATCGCTCCAAAAAGCAAGATTCGGAAACTTC	500
84	lnIleArgAsnIleProProHisLeuGlnTrpGlnValLeuAspSerLeu	100
501	AGATACGAATATCCGCCCTCATTTACAGTGGGAGGTCTGGATAGTTA	550
101	LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe	117
551	CTAGTCCAGTATGAGTGTGTGAGAGCTGTGAGCAAGTGAACACTGACT	600
117	rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG	134
601	GGAAACTGCAAGTTGAATGTAACTATTCCAGTAAGGACCAAGCTAGAC	650
134	lnAlaLeuAspLysLeuAsnGlyPheGlnLeuGlnAsnPheThrLeuLys	150
651	AGGCACCTAGACAACCTGAATGGATTTTCAGTTAGAGATTTTCACCTT	700
151	ValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnI	167
701	GTAGCCTATATCCCTGATGAAATGGCGCCACGACAAACCCCTTGACGA	750
167	nProArgGlyArgArgGlyLeuGlnArgGlySerSerArgGlnGlyS	184
751	GCCCCGAGGTGCGCGGGGCTTGGGACAGAGGGCTCCTCAAGGACGAGG	800
184	erProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu	200
801	CTCCAGGATCCGATCCACAGAACCATGTGATTTGCCCTCTGCCCTG	850
201	LeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaTh	217
851	CTGTTCCCAACCAATTTGTTGGGCCATCATAGGAAAAAGAGTGCAC	900
217	rIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgL	234
901	CATTTCGGAACATCACCAACAGACCCAGTCTAAATCGATGTCCACCGTA	950
234	ysGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrPro	250
951	AGAAAAATGCGGGGCTCTGAGAGTCTGATTTACTTCTCTCTACTCT	1000
251	GluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMethisLysG	267
1001	GAAGGCACCTCTCGGGCTTCTAAGTCTATTCTGAGATTATGCATAAGGA	1050
267	uAlaGlnAspIleLysPheThrGluGluIleProLeuLysIleLeuAlaH	284
1051	AGCTCAAGATATAAAATTCACAGAAGAGATCCCTTTGAAGATTTTAC	1100
284	isAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLys	300
1101	ATAATACTTTGTTGGACGCTTATTGGTAAGAAGAGAAATCTTAA	1150
301	LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnI	317

1151	AAAAATTGACCAAGACACACAGACACTAAAATCACGATATCTCCATTGCGAGGA	1200
317	uLeuThrLeuTyrAsnProGluAArgThrIleThrValLysGlyAsnValG	334
1201	ATTGACCGCTGTATTAATCCAGAACCCACTATTACAGTTAAAGGCAATGTTG	1250
334	luThrCysAlaLysAlaGluGluGluIleMethLysLysIleArgGluSer	350
1251	AGACATGTGCCAAAGCTGAGGAGGAGATCATGAAGAAAAATCAGGGAGTCT	1300
351	TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProG1	367
1301	TATGAAATGATATTGCTCTATGAACTTCAACGACATTTAATTCCTGG	1350
367	YLeuAsnLeuAsnAlaLeuGlyLeuPheProThrSerGlyMetProp	384
1351	ATTAAATCTGAACGCGTTGGTCTGTTCCCAACCACCTTCAGGGATGCCAC	1400
384	roProThrSerGlyProProSerAlaMethThrProProTyrProGlnPhe	400
1401	CTCCCAACCTCAGGGCCCGCTTCAGCCATGACTCTCCCTACCCGCGAGTTT	1450
401	GluGlnSerGluThrGluThrValHisGlnPheIleProAlaLeuSerVa	417
1451	GAGCAATCAGAAACGGAGACTGTTTCATCAGTTTATCCAGCTCTATCAGT	1500
417	IcIyAlaIleIleGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgp	434
1501	CGGTGCCATCATCGGCAAGCAGGCGCCAGCACATCAAGCAGCTTTCGCT	1550
434	heAlaGlyAlaSerIleLysIleAlaProAlaGluAlaProAspAlaLys	450
1551	TTGCTGGAGCTTCANTTAAGATTGCTCCAGCGGAAGCACCATGCTATAA	1600
451	ValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaG1	467
1601	CTGAGGATGGTCATTATTCATCTGGACCAACCAGAGCGCTCAGTTCAAGGCTCA	1650
467	nGlyArgIleTyrGlyLysIleLysGluGluAsnPheValSerProLysG	484
1651	GGGAGAATTTATGGAAAAATTAAGAAAGAAACTTTGTAGTCCTAAAG	1700
484	luGluValLysLeuGluAlaHisIleArgValProSerPheAlaAlaGly	500
1701	AAGAGGTGAAACTTGAAGCTCATATCAGAGTGCCATCCTTTGCTGTGGC	1750
501	ArgValIleGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuSe	517
1751	AGAGTTATTGGAAAAGGAGGCAAAACGGTGAATCAACTTCAGAAATTTGTC	1800
517	rSerAlaGluValValProArgAspGlnThrProAspGluAsnAspG	534
1801	AAGTCGAAGCTGTTGTCCTCGTGACCACACACCTGATGAGATGACC	1850
534	InValValValLysIleThrGlyHisPheTyrAlaCysGlnValAlaGln	550
1851	AAGTGGTTGTCAAAAATACTGGTCACTCTATGCTGCCAGGTGCCAC	1900
551	ArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnGlnLy	567
1901	AGAAAAATTCAGAAATTTCTGACTCAGGTAAAGCAGCACCAACACAGAA	1950
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seq_documentation_block:
; Sequence 175, Application US/09850716
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 175
LENGTH: 4181
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (3347)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3502)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3506)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3520)
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NAME/KEY: unsure
LOCATION: (3538)
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NAME/KEY: unsure
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NAME/KEY: unsure
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LOCATION: (4062)
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NAME/KEY: unsure
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NAME/KEY: unsure
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NAME/KEY: unsure
LOCATION: (4115)
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US-09-850-716-175

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Ratio: 5.105 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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Align seg 1/1 to: US-09-850-716-175 from: 1 to: 4181

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17 pleuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
|||||
301 CCTGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTGCGGACCTTCC 350
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
|||||
351 TGGTGAAGACTGGCTACGCGTTCTGGACTGCCCGGACGAGAGCTGGGCC 400
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
|||||
401 CTCAGGGCCATCGAGCGCGTTTCAGGTAAATAGAACTGCACGGGAAACC 450
67 oIleGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
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451 CATAGAAGTTGAGCACTCGGTCCCAAAAGGCAAGGATTCCGGAACATTC 500
84 InIleArgAsnIleProHisLeuGlnTrpGluValLeuAspSerLeu 100
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501 AGATACGAAATATCCCGCTCATTTACAGTGGAGGTGCTGGATAGTTTA 550
101 LeuValGlnTyrGlyValGluSerCysGluGlnValAsnThrAspSe 117
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551 CTAGTCCAGTATGGAGTGTGGAGAGCTGTGAGCAAGTGAACACTGACTC 600
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601 GGAAACTGCAGTTGTAATGTAACTTATTCAGTAAGGACCAAGCTAGAC 650
134 InAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLys 150
|||||
651 AAGCACTAGACAAACTGAATGGATTTCAGTTAGAGAAATTTACCTTGAAA 700
151 ValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnGl 167
|||||
701 GTAGCTATATCCCTGATGAAATGGCGCCAGCAAAACCCCTTCAGCA 750
167 nProArgGlyArgArgGlyLeuGlyGlnArgLysSerArgGlnGlyS 184
|||||
751 GCCCGAGGTCCCGGGGGCTTGGGCAGAGGGGCTCTCAAGGCAGGGGT 800
184 erProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu 200
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801 CTCAGGATCGGTATCCAGCAGAGAAACCATGTGATTGCTCTCGCGCTG 850
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217 rIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgL 234
|||||
901 CATTCGGAACATCACCAACAGACCCAGCTCTAAATCGATGTCCACCGTA 950
234 yGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrPro 250
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951 AAGAAATGCGGGGCTGCTGAGAAAGTCGATTACTATCTCTCTACTCT 1000
251 GluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLysGl 267

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1001 GAAGGCACCTCTGCGCTTGTAAAGTCTATTCTGGAGATTATGCATAAGGA 1050
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301 LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnG 317
|||||
1151 AAATTCACAGACACACACACTAAATCAAGATATCCTCATTCAGGA 1200
317 uLeuThrLeuTyrAsnProGluGluArgThrIleThrValLysGlyAsnValG 334
|||||
1201 ATTGACCGCTGTATATCCAGAAGCGCACTATTACAGTTAAAGGCAATGTTG 1250
334 luThrCysAlaLysAlaGluGluGluIleMetLysLysIleArgGluSer 350
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1251 AGACATGTGCCAAGCTGAGGAGGAGATCATGAAGAAATCAGGGAGTCT 1300
351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisIleProG 367
|||||
1301 TATGAAATGATATTGCTTCTATGAATCTTCAAGCACATTTAATTCCTGG 1350
367 yLeuAsnLeuAsnAlaLeuGlyLeuPheProThrSerGlyMetProp 384
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1351 ATTTAAATCTGAAGCCCTTGGGCTGTTCACCACCCACTTCAGGGATGCCAC 1400
384 roProThrSerGlyProProSerAlaMetThrProProTyrProGlnPhe 400
|||||
1401 CTCCACCTCAGGGCCCTTTCAGCCATGACTCTCCCTACCGCAGTTT 1450
401 GluGlnSerGluThrGluThrValHisGlnPheIleProAlaLeuSerVa 417
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1451 GACCAATCAGAACGGAGAGCTGTTCATCAGTTATCCACAGCTCTATCAGT 1500
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1501 CGGTGCCATCATCGGCAAGCAGGCGCCAGCACATCAAGCAGCTTTCCTCGCT 1550
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451 ValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaG 467
1601 GTGAGGATGCTGATTATCATTGACCCAGCAGAGGCTCAGTTCAAGGCTCA 1650
467 nGlyArgIleTyrGlyLysIleLysGluGluAsnPheValSerProLysG 484
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501 ArgValIleGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuSe 517
1751 AGAGTTTATGGAAAAAGGCGCAAAACGGTGAATGAACCTTCAGAAATTTGTC 1800
517 rSerAlaGluValValProArgAspGlnThrProAspGluAsnAspG 534
1801 AAGTGCAGAGTGTGTTGCTCCTCGTCACAGACACCTGATGAGAATGACC 1850
534 lnValValValLysIleThrGlyHisPheTyrAlaCysGlnValAlaGln 550
1851 AAGTGTGTGCAAAATAACTGGTCACTTCTATGCTTGCAGGAGTTGCCAG 1900
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1951 GGCTCTGCAAGTGGACCACTCAGTCAAGACGGAAG 1987
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; Sequence 145, Application US/60281593
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 P
; CURRENT APPLICATION NUMBER: US/60/281.593
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 145
; LENGTH: 4434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1383415.3
; NAME/KEY: unsure
; LOCATION: 2203
; OTHER INFORMATION: a, t, c, g, or other
; US-60-281-593-145
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Ratio: 5.095          Gaps: 0
Percent Similarity: 99.827 Percent Identity: 99.655
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17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
302 CCTAGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTCGGGACCTTC 351
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
352 TGCTGAAGACTGGCTACGCGTTGCTGACTGCCCGGACGAGAGCTGGCC 401
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
402 CTCACGGCCATCGAGCGCTTTTCAGTAAATAGAACTGCACGGGAACC 451
67 oileGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
452 CATAGAAGTTGAGCACTCGGTCCCAAAAGGCAAGGATTCGGAACCTTC 501
84 lnIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
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552 CTAGTCCAGTATCGAGTGTGGAGCTGTGACCAAGTGAACACTGACTC 601
117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArg 134
602 GGAACCTGCAGTTGTAATGTAACTTATCCAGTAAGACCAAGCTAGAC 651
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134 InAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLys 150
152 AAGCACTAGACAACTGAATGATTTCACTTTAGAGAAATTCACCTTGAAA 701
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702 GTAGCCTATATCCCTGTGTAATGGCCGCCAGCAAAACCCCTTGCGACA 751
167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGlyS 184
752 GCCCGAGGTGCGCGGGGCTGGGCCAGAGGGCTCCTCAAGGCAGGGGT 801
184 erProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu 200
802 CTCACAGGATCCGTATCCAAGCAGAAACCATGTGATTTGCTCTGCGCTG 851
201 LeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaTh 217
852 CTGGTTCACCAATTTGTTGGAGCCATCATAGGAAAGAGGTGGCCAC 901
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902 CATTCGGAACATCACCAACACACCGCTGTAATTCGATGTCACCGTA 951
234 yGluAsnAlaGlyAlaIleGlySerIleThrIleLeuSerThrPro 250
952 AAGAAATTCGCGGGCTGCTGAGAAAGTCGATTACTCTCTACTCT 1001
251 GluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLysG 267
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284 IsAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLys 300
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; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
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317 uLeuThrLeuTyrAsnProGluArgThrIleThrValLysGlyAsnValG 334
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; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.

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; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606, 421A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
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; US-09-606-421A-347

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About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

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seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-510-376A-175

seq_documentation_block:

; Sequence 175, Application US/09510376A

; GENERAL INFORMATION:

; APPLICANT: Wang, Tonglong

; APPLICANT: Fan, Liqun

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; FILE OF INVENTION: 210121.455C7

; CURRENT APPLICATION NUMBER: US/09/510,376A

; NUMBER OF SEQ ID NOS: 330

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 175

; LENGTH: 4181

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)-(4181)

; OTHER INFORMATION: n=A,T,C or G

US-09-510-376A-175

alignment_scores:

Quality: 2956.00 Length: 579

Ratio: 5.105 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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67 olleGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84

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451 CATAGAAGTTGAGCAGCTCGGTCCCAAGGATTCGGAAGCTTC 500

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84 InileArgAsnIleProPheHisLeuGlnTrpGluValLeuAspSerLeu 100

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101 LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe 117

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117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG 134

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1001 GAAGCACCTCTCGGCTTGTAACTATTCTGGAGATTATGCATAAGCA 1050
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; Sequence 21954, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 21954
; LENGTH: 4264
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1774)..(2013)
; OTHER INFORMATION: 55% homologous to Homo sapiens IGF-II mRNA-binding protein
; OTHER INFORMATION: 3, accession number AF117108, Smith-Waterman Score=204.
PCT-US01-08631-21954
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Ratio:	4.744	Gaps:	9
Percent Similarity:	96.441	Percent Identity:	93.898

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1791 TTTGTTAGTCTTAAGAGAGAGTGAACCTTGAAGCTCATATCAGAGTGCC 1840
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2091 GGAAG 2095


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463 nPheLysAlaGlnGlyArgIleThrGlyLysIleLysGluAsnPheV 480
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530 spGluAsnAspGlnValValValLysIleThrGlyHisPheTyrAlaCys 546
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547 GlnValAlaGlnArgLysIleGlnGluIleLeuThrGlnValLysGlnH1 563
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seq_name: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:PCT-US01-08631-6785

seq_documentation_block:
; Sequence 6785, Application PC/TUS0108631
; GENERAL INFORMATION:

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; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 6785
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (50)..(1843)
; OTHER INFORMATION: 100% homologous to Homo sapiens IGF-II mRNA-binding protein
; OTHER INFORMATION: 2.accession number AF117107,Smith-Waterman Score=3059.
PCT-US01-08631-6785

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alignment_scores:
Quality: 1950.50 Length: 591
Ratio: 3.817 Gaps: 8
Percent Similarity: 86.464 Percent Identity: 65.313

alignment_block:

US-09-466-396a-176 x PCT-US01-08631-6785 ..

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||||| 34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
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||||| 51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
||||| 200 ATCCGCGCCATCGAGACCTCTCGGTAAGTGAATGTCATGGGAAAT 249
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||||| 101 LeuValGlnThrGlyValValGluSerCysGluGlnValAsnThrAspSe 117
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889 ATTCTCATCCCGGATGAGAGGTGAGCTCCCTTCGCCCTCAG... 936
167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGly. 183
937 ....CGAGCCAGCGT.....GGGACCACTCTTCCGGGAGAGGCC 976
184 ..SerProGlySerValSerLysGlnLysProCysAspLeuProLeuArg 199
977 ACCCCCTGGGGGACATCTTCAGCCGACAGACAGATTGATTTCCCGCTGCGG 1026
200 LeuLeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAl 216
1027 ATCTGTGTCCCAACCAGTTGTGTGTGCCATCATCGGAAGAGGCGTT 1076
216 aThrIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHis 233
1077 GACCATAAAGAACATCACTAAGCAGACCCAGTCCCGGTAGATATCCATA 1126
233 rGlyGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThr 249
1127 GAAAGAGAACTCTGGAGCTGCAGAGGCTGTCCACCATCCATGCCACC 1176
250 ProGluGlyThrSerAlaLacLysSerIleLeuGluIleMethIstY 266
1177 CCAGAGGGACTTCTGAGCATCCCGCATGATCTTGAAATCATGTCAGAA 1226
266 sGluAlaGlnAspIleLysPheThrGluGluIleProLeuLysIleLeu 283
1227 AGAGCAGATGAGACAAACTAGCCGAGAGATTCCTCTGAAATCTTGG 1276
283 laHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeu 299
1277 CACACAATGGCTTGGTGGAGACTGATTGGAAAGAGGACAGAAATTTG 1326
300 LysLysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuG 316
1327 AAGAAATGAAATGAACATGAACAGGACCAAGATACAAATCTCATCTTGC 1376
316 nGluLeuThrLeuThrAsnProGluArgThrIleThrValLysGlyAsn 333
1377 GGATTTGAGCATATACAAACCGGAAAGAACCACTCACTGTGAAGGCCAC 1426
333 alGluThrCysAlaLysAlaGluGluIleMetLysLysIleArgGlu 349
1427 TTGAGGCTGTCCAGTGTGATAGATAGATATGAAGAGCTGCTGAG 1476
350 SerTyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIle 366
1477 GCCTTTGAAATGATATGCTGGCTGTACACCCACTCC..... 1515
366 oGlyLeuAsnLeuAsnAlaLeuGlyLeuPheProProThrSerGlyMet 383
1516 .....TCCACTTTC.....GCATACTTC..... 1524
383 roProProThrSerGlyProProSerAlaMetThrProProThrProGln 399
1525 .....TCCAGCCTGTACCCCATCACAGTTTGGCCCGCTTCCCGCAT 1566
400 PheGluGln...SerGluThrGluThrValHisGlnPheIleProAla 415
1567 CATCACTCTTATCCAGAGAGGAGATGTGAATCTCTTCAATCCCAACCCA 1616
415 uSerValGlyAlaIleIleGlyLysGlnGlnHisIleLysGlnLeuS 432
1617 GGCTGTGGGCGCCATCATCGGAAGAAGGGGCACACATCAACAGCTGG 1666
432 erArgPheAlaGlyAlaSerIleLysIleAlaProAlaGluAlaProAs 448
1667 CGAGATTTCGGCGGAGCTCTATCAAGATTGCCCTCGCGAAGGCCAGAC 1716
449 AlaLysValArgMetValIleIleThrGlyProProGluAlaGlnPhe 465
1717 GTCAGGAAAGGATGGTCATCATCACCGGGCCACCGAAGCCAGTTCAA 1766

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465 sAlaGlnGlyArgIleTyrGlyLysIleLysGluGluAsnPheValSerP 482
1767 GGCCCAAGGACGATCTTGGGAACTGAAAGAGGAAACTTCTTTAAAC 1816
482 rGlyGluGluValLysLeuGluAlaHisIleArgValProSerPheAla 498
1817 CCAAGAAAGTGAAGCTGGAAGCGCATATCAGATGCCCTCTTCCACA 1866
499 AlaGlyArgValIleGlyLysGlyGlyLysThrValAsnGluLeuGln 515
1867 GCTGGCCGGGTGATTGGCAAGGTGGCAACCGTGAACCACTGCAGAA 1916
515 nLeuSerSerAlaGluValValProArgAspGlnThrProAspGlu 532
1917 CTTAAACAGTGCAGAGTCATCGTGCCTCGTCAACCAACGCCAGATGAA 1966
532 sAspGlnValValValLysIleThrGlyHisPheTyrAlaCysGlnVal 548
1967 ATGAGGAAGTGCATCGTCAAGAAATTATCGGGCCTCTTTGTAGCCAG 2016
549 AlaGlnArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGln 565
2017 GCACAGCGCAAGATCAGGGAATTTGTACAACAGGTGAAGCAGCAGG 2066
565 nGln 566
2067 GAAA 2070

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seq_name: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq: PCT-US01-08631-21952

seq_documentation_block:

; Sequence 21952, Application PC/TUS0108631

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 21272-049

; CURRENT APPLICATION NUMBER: PCT/US01/08631

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 21952

; LENGTH: 1998

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIMILAR

; LOCATION: (3)..(179)

; OTHER INFORMATION: 94% homologous to Homo sapiens IGF-II mRNA-binding protein

; OTHER INFORMATION: 3.accession number AF117108,Smith-Waterman Score=293.

; PCT-US01-08631-21952

alignment_scores:

Quality: 776.50

Ratio: 3.806

Percent Similarity: 36.691

Length: 556

Gaps: 3

Percent Identity: 34.712

alignment_block:

US-09-466-396A-176 x PCT-US01-08631-21952

Align seg 1/1 to: PCT-US01-08631-21952 from: 1 to: 1998

24 AspAlaLysIleProValSerGlyProPheLeuValLysThrGlyTyrAl 40

3 GAGCCCAAGATCCCGTGTCCGGACCCCTTCTTGTGAAGATTGGCTAGCG 52

40 aPheValAspCysProAspGluSerTrpAlaLeuLysAlaIleGluAla 57

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53 GTTCGTGGACTCCAGACAGCATCTGGCCCTCAAGGCCATTGAGGCC 102
57 euserGlyLysIleGluLeuHisGlyLysProIleGluValGluHisSer 73
103 TTTTCAGGTAATAAGTACAGTGCACGGGAACCCATAGAAATTGAGCACATCG 152
74 ValProLysArgGlnArgIleArgLysLeuGlnIleArgAsnIlePro 90
153 GTCCCAAAAGGCAAGGATTGCA
90 oHisLeuGlnTrpGluValLeuAspSerLeuValGlnTyrGlyVal 107
176 ..... 176
107 aIgluSerCysGluGlnValAsnThrAspSerGluThrAlaValValAsn 123
176 ..... 176
124 ValThrTyrSerSerLysAspGlnAlaArgGlnAlaLeuAspLysLeuAs 140
176 ..... 176
140 nGlyPheGlnLeuGluAsnPheThrLeuLysValAlaTyrIleProAspG 157
176 ..... 176
157 luMetAlaAlaGlnGlnAsnProLeuGlnGlnProArgGlyArgArgGly 173
176 ..... 176
174 LeuGlyGlnArgGlySerSerArgGlnGlySerProGlySerValSerly 190
176 ..... 176
190 sGlnLysProCysAspLeuProLeuArgLeuValProThrGlnPheV 207
176 ..... 176
207 alGlyAlaIleIleGlyLysGluGlyAlaThrIleArgAsnIleThrLys 223
176 ..... 176
224 GlnThrGlnSerLysIleAspValHisArgLysGluAsnAlaGlyAlaAl 240
177 .....GAAATGCGAGGGCTGC 193
240 aGluLysSerIleThrIleLeuSerThrProGluGlyThrSerAlaAlaC 257
194 TGAGAAGTCGATTACTCTCTCTACTCTCTGAGGCACCTCTGCGGCTT 243
257 ysLysSerIleLeuGluIleMetHisLysGluAlaGlnAspIleLysPhe 273
244 GTAAGTCTATTCTGGAGATTATGCGTAAGGAACCTCAAGATGTAATAATTC 293
274 ThrGluGluIleProLeuLysIleLeuAlaHisAsnAsnPheValGlyAr 290
294 ACAGAAGAGATCCCTTG
290 gluIleGlyLysGluGlyArgAsnLeuLysLysIleGluGlnAspThrA 307
311 ..... 311
307 spThrLysIleThrIleSerProLeuGlnGluLeuThrLeuTyrAsnPro 323
311 ..... 311
324 GluArgThrIleThrValLysGlyAsnValGluThrCysAlaLysAlaGl 340
311 ..... 311
340 uGluGluIleMetLysLysIleArgGluSerTyrGluAsnAspIleAlas 357
311 ..... 311
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357 erMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsnLeuAlaLeu 373
311 ..... 311
374 GlyLeuPheProProThrSerGlyMetProProProThrSerGlyProPr 390
311 ..... 311
390 oSerAlaMetThrProProTyrProGlnPheGluGlnSerGluThrGluT 407
311 ..... 311
407 hrValHisGlnPheIleProAlaLeuSerValGlyAlaIleIleGlyLys 423
312 .....TTTATCCGGCTCTATCAGTCAGAGCCCTCATCAGCAAG 350
424 GlnGlyGlnHisIleLysGlnLeuSerArgPheAlaGlyAlaSerIleLy 440
351 CAGGCCACAGCACATCAAGCAGCTTTCTCGCTTTGCTGGAGCTTCAAGTAA 400
440 sIleAlaProAlaGluAlaProAspAlaLysValArgMetValIleIleT 457
401 GATTCTCCAGTGGAGGCCAGATGCTAAGGTGAGGATGGTGATGATCG 450
457 hrGlyProProGluAlaGlnPheLysAlaGlnGlyArgIleTyrGlyLys 473
451 CTGGATCACCATGTTGT
474 IleLysGluGluAsnPheValSerProLysGluGluValLysLeuGluAl 490
467 ..... 467
490 aHisIleArgValProSerPheAlaAlaGlyArgValIleGlyLysGlyG 507
467 ..... 467
507 lyLysThrValAsnGluLeuGlnAsnLeuSerSerAlaGluValVal 523
467 ..... 467
524 ProArgAspGlnThrProAspGluAsnAspGlnValValValLysIleTh 540
468 .....GACCAGACACCTGATGAGATGACCAAGTGGTGTCAAAATAAC 511
540 rGlyHisPheTyrAlaCysGlnValAlaGlnArgLysIleGlnGluIleL 557
512 TGGTCACCTTCTATGCTTCCAGGTTGCCAGAGAAAATTCAGGAAATTC 561
557 euThrGlnValLysGlnHisGlnGlnLysAlaLeuGlnSerGlyPro 573
562 TGACTCAGGTAAAGCAGCAGCAACAACAGAGGCTCTGCAAAAGTGACCA 611
574 ProGlnSerArgArgLys 579
612 CCTCAGTCAAGACGGAAG 629
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seq_name: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:PCT-US01-08631-12584

seq_documentation_block:
; Sequence 12584, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom

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; SEQ ID NO 12584
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (3)..(1469)
; OTHER INFORMATION: 31% homologous to Herpesvirus papio NTR, accession number
; OTHER INFORMATION: AF200364, Smith-Waterman Score=247.
PCT-US01-08631-12584

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alignment_scores:
  Quality: 775.50      Length: 558
  Ratio: 3.783        Gaps: 3
  Percent Similarity: 36.738  Percent Identity: 34.588

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alignment_block:

US-09-466-396A-176 x PCT-US01-08631-12584 ..

Align seg 1/1 to: PCT-US01-08631-12584 from: 1 to: 1998

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21 ILePheLysAspAlaLysIleProValSerGlyProPheLeuValLysTh 37
||||:|||||
3 ATCTGAAGGACGCCAAGATCCCGTCTCGGACCTTCTCGTGAAGAT 52
||||:|||||
37 rGlyTyrAlaPheValAspCysProAspGluSerTrpAlaLeuLysAlaI 54
||||:|||||
53 TGGCTACGCGTCTGCTGACTGCCACAGAGATCTGGGCCCTCAAGGCCA 102
||||:|||||
54 leGluAlaLeuSerGlyLysIleGluLeuHisGlyLysProIleGluVal 70
||||:|||||
103 TTGAGGCGCTTCAGGTAAATAAGACTGCACGGGAACCATAGAAGTT 152
||||:|||||
71 GluHisSerValProLysArgGlnArgIleArgLysLeuGlnIleArgAs 87
||||:|||||
153 GACCACTCGGTCCCAAAAGGCAC..... 176
87 nIleProHisLeuGlnTrpGluValLeuAspSerLeuLeuValGlnT 104
176 ..... 176
104 yRGlyValValGluSerCysGluGlnValAsnThrAspSerGluThrAla 120
176 ..... 176
121 ValValAsnValThrTyrSerSerLysAspGlnAlaArgGlnAlaLeuAs 137
176 ..... 176
137 pLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysValAlaTyrI 154
176 ..... 176
154 leProAspGluMetAlaAlaGlnGlnAsnProLeuGlnGlnProArgGly 170
176 ..... 176
171 ArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGlySerProGlyse 187
176 ..... 176
187 rValSerLysGlnLysProCysAspLeuProLeuArgLeuValProt 204
176 ..... 176
204 hrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaThrIleArgAsn 220
176 ..... 176
221 ILeThrLysGlnThrGlnSerLysIleAspValHisArgLysGluAsnAl 237
||||:|||||
177 .....CACCGTAAAGAAATGC 193

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```

237 aGlyAlaAlaGluLysSerIleThrIleLeuSerThrProGluGlyThrS 254
||||:|||||
194 AGGGCTGCTGAGAAGTCGATTACTATCTCTACTCTCTGAAGGCACCT 243
||||:|||||
254 erAlaAlaCysLysSerIleLeuGluIleMetHisLysGluAlaGlnAsp 270
||||:|||||
244 CTCGGCTTCAAGTCTATTCTGGAGATTATGCGTAAAGAACTCAAGAT 293
||||:|||||
271 ILeLysPheThrGluGluIleProLeuLysIleLeuAlaHisAsnAspPh 287
||||:|||||
294 GTAAATTCACAGAAGT..... 311
287 eValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLysLysIleGluG 304
||||:|||||
311 ..... 311
304 lNAspThrAspThrLysIleThrIleSerProLeuGlnGluLeuThrLeu 320
||||:|||||
311 ..... 311
321 TyrAsnProGluArgThrIleThrValLysGlyAsnValGluThrCysAl 337
||||:|||||
311 ..... 311
337 aLysAlaGluGluIleMetLysLysIleArgGluSerTyrGluAsnA 354
||||:|||||
311 ..... 311
354 spIleAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsnLeu 370
||||:|||||
311 ..... 311
371 AsnAlaLeuGlyLeuPheProThrSerGlyMetProProThrSe 387
||||:|||||
311 ..... 311
387 rGlyProProSerAlaMetThrProProTyrProGlnPheGluGlnSerG 404
||||:|||||
311 ..... 311
404 luThrGluThrValHisGlnPheIleProAlaLeuSerValGlyAlaIle 420
||||:|||||
312 .....GTTCATCTGTTTATCCCGCTCTATCAGTCAGAGCCCTC 350
||||:|||||
421 ILeGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgPheAlaGlyAl 437
||||:|||||
351 ATCAGCAAGCAGGCGCCACACATCAACAGCAGCTTCTCGCTTGTGGAGC 400
||||:|||||
437 aSerIleLysIleAlaProAlaGluAlaProAspAlaLysValArgMetV 454
||||:|||||
401 TTCAAGTAAGATTGCTCCAGTGGGAAGCACCAGATGCTAAGGTGAGGATGG 450
||||:|||||
454 alIleIleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArgIle 470
||||:|||||
451 TGATGATCGCTGCT..... 464
471 TyrGlyLysIleLysGluGluAsnPheValSerProLysGluGluValLy 487
464 ..... 464
487 sLeuGluAlaHisIleArgValProSerPheAlaAlaGlyArgValIleG 504
464 ..... 464
504 lLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuSerSerAlaGlu 520
464 ..... 464
521 ValValValProArgAspGlnThrProAspGluAsnAspGlnValValVa 537
||||:|||||
465 ...GTTCTCCCTTGTGACCACACACCTGATGAGAATGACCAAGTGGTGT 511

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537 llystlethrGlyHisPheTyrAlaCysGlnValAlaGlnArgLysIleG 554
|||||
512 CAAATAAAGTGTCTACTTCTATGCTTGCAGGTGCCAGAGAAAATTC 561
|||||
554 InGluIleLeuThrGlnValLysGlnHisGlnGlnGlnLysAlaLeuGln 570
|||||
562 AGGAATTTCTGACTCAGGTAAAGCAGCAGCAACACAGAGGCTCTGCA 611
|||||
571 SerGlyProGlnSerArg 578
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612 ACTGGACCACCTCAGTCAAGACGG 635
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seq_name: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq: PCT-US01-08631-21953

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seq_documentation_block:
; Sequence 21953, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 21953
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (4)..(333)
; OTHER INFORMATION: 98% homologous to Mus musculus igf2 mRNA-binding protein
; OTHER INFORMATION: 3, accession number AB046173, Smith-Waterman Score=541.
PCT-US01-08631-21953
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Quality: 537.00 Length: 118
Ratio: 4.752 Gaps: 1
Percent Similarity: 95.763 Percent Identity: 94.068
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alignment_block:
US-09-466-396A-176 x PCT-US01-08631-21953 ..

Align seg 1/1 to: PCT-US01-08631-21953 from: 1 to: 456

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4 CAATCAGAAACGAGACTGTTTCATCTGTTATCCAGCTCTATCAGTCGG 53
|||||
418 ValAlaIleGlyLysGlnGlyGlnHisThrLysGlnLeuSerArgPheA 435
|||||
54 TCCCATCATCGGCAAGCAGGCCACATCAAGCAGCTTCTCGCTTG 103
|||||
435 laGlyAlaSerIleLysIleAlaProAlaGluAlaProAspAlaLysVal 451
|||||
104 CTGGAGCTTCATTAAAGATTGCTCCAGCGGAGCACCAGATGCTAAAGTG 153
|||||
452 ArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaGlnG1 468
|||||
154 AGGATGGTGATTATACATCGACACACAGAGGCTCAGTTCAAGGCTCAGG 203
|||||
468 VargIleTyrGlyLysIleLysGluGluAsnPheValSerProLysGluG 485
|||||
204 AGCAATTTATGGAATAAATAAGAGAAACCTTTGTTAGTCTCTAAAGAG 253
|||||
485 luValLysLeuGluAlaHisIleArgValProSerPheAlaAlaGlyArg 501
|||||
254 AGGTGAACCTGAAGCTCATATCAGAGTGCCATCCTTTGCTGCTGGCAGA 303
|||||
```

```
502 ValIleGlyLysGlyLysThrValAsnGlu.LeuGlnAsnLeuSerS 518
|||||
304 GTTATTGGAAGAGGCAACACGCAAGTACTTCAGCAAAACCTGTGCA 353
|||||
518 er 518
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354 GT 355
|||||
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seq_name: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq: US-60-253-652-10626

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seq_documentation_block:
; Sequence 10626, Application US/60253652
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: tissues and methods for their use.
; FILE REFERENCE: 1055P2
; CURRENT APPLICATION NUMBER: US/60/253,652
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29954
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10626
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Bovine
; US-60-253-652-10626
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Ratio: 3.912 Gaps: 1
Percent Similarity: 73.469 Percent Identity: 61.224
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alignment_block:
US-09-466-396A-176 x US-60-253-652-10626 ..

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44 CAGCACTGTGCCATCTTCTCTCGGGCTCCTGCCATCTCTTGGGGCGGCGAG 93
|||||
442 aProAlaGluAlaProAspAlaLysValArgMetValIleIleThrGlyP 459
|||||
94 GCCACCATCAGCGCGCAGATGTATCCTGCAGAGGCTGCTCCCGTGGGCG 143
|||||
459 roProGlu..... 461
||
144 CAGGCCATTAACTTTTACCCTGTAAATCAGTCAACCTTTGGCCTTTCC 193
|||||
462 .....AlaGlnPheLysAlaGlnGlyAr 469
|||||
194 TACCTGAATGACACTGATAGGCTATGTTCTCATCTGTAGGCTCAGGGAAG 243
|||||
469 gIleTyrGlyLysIleLysGluGluAsnPheValSerProLysGluGluV 486
|||||
244 AATTATTGAAAAAATAAAGAAGAAAAATTTGTTAGTCTCTAAAGAAGAGG 293
|||||
486 alLysLeuGluAlaHisIleArgValProSerPheAlaAlaGlyArgVal 502
|||||
294 TGAACCTTTGAAGCTCACATCAGAGTGGCTCTTTGCTGCTGGCAGAGTT 343
|||||
503 IleGlyLysGlyLysThrValAsnGluLeuGlnAsnLeuSerSerAl 519
|||||
344 ATTGGAAGAGGAGCAACCGTGAATCAGCTCCAGATTTGTCAGGTGC 393
|||||
519 aGluValValValProArgAspGlnThrProAspGluAsnAspGlnValV 536
|||||
394 AGAAGTTGTTGTTCCCGCTGACCAGACTCCTGATGAGAATGACCAGGTGG 443
|||||
536 alValLysIleThrGlyHisPheTyrAlaCysGlnValAla 549
|||||
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444 TCGTCAGATAACTGGTCACCTTCTATCTGCTGCCAGGCAAGT 484
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seq_documentation_block:
; Sequence 21454, Application US/60253652
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: tissues and methods for their use.
; FILE REFERENCE: 1055p2
; CURRENT APPLICATION NUMBER: US/60/253,652
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29954
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21454
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Bovine
US-60-253-652-21454

alignment_scores:
  Quality: 401.00      Length: 91
  Ratio: 4.557        Gaps: 0
  Percent Similarity: 96.703  Percent Identity: 86.813

alignment_block:
US-09-466-396A-176 x US-60-253-652-21454 ..
Align seg 1/1 to: US-60-253-652-21454 from: 1 to: 273
429 lysGlnLeuSerArgPheAlaGlyAlaSerIleLysIleAlaProAlaG1 445
1 ARGAGCTCTCCGGTTCGCCAGGCGCTCCATCAAGATTGCTCTCTGA 50
445 uAlaProAspAlaLysValArgMetValIleIleThrGlyProProGluA 462
51 AACTCCAGACTCCAAGTTCGTATGTTGTCATCATCTACCTGGAGCCGCCAAG 100
462 laGlnPheLysAlaGlnGlyArgIleThrGlyLysIleLysGluGluAsn 478
101 CCCAGTTCAGGCTCAGGGAAGAATTATGGAAACTCAAGGAGGAGAAC 150
479 PheValSerProLysGluGluValLysLeuGluAlaHisIleArgValPr 495
151 TTCCTTGGTCCCAAGGAGAGTAAGTAACTGGAGCCCATATCCGGGTGCC 200
495 oSerPheAlaAlaGlyArgValIleGlyLysGlyLysThrValAsnG 512
201 AGCGTCAGCAGCGCGCGGTTCATTGGCAAGSTGGCAAGACGGTGAATG 250
512 luLeuGlnAsnLeuSerSerAla 519
251 AGCTGCAAAATTTGACAGCAGCT 273

seq_name: /cgn2_6/ptodata/2/pna/us60_NEW_COMB.seq:US-60-278-232-4474
seq_documentation_block:
; Sequence 4474, Application US/60278232
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preethi
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence databases, and Single Nucleotide
; TITLE OF INVENTION: Polymorphisms Identified Thereby
; FILE REFERENCE: GX-0011 P
; CURRENT APPLICATION NUMBER: US/60/278,232
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12,557

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; SOFTWARE: PERL Program
; SEQ ID NO 4474
; LENGTH: 4628
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 234498.6
; NAME/KEY: unsure
; LOCATION: 2161
; OTHER INFORMATION: a, t, c, g, or other
US-60-278-232-4474

alignment_scores:
  Quality: 235.50      Length: 449
  Ratio: 1.056        Gaps: 18
  Percent Similarity: 49.666  Percent Identity: 22.272

alignment_block:
US-09-466-396A-176 x US-60-278-232-4474 ..
Align seg 1/1 to: US-60-278-232-4474 from: 1 to: 4628
161 GlnGlnAsnProLeuGln.....GlnProArgGlyArgArgGlyLe 174
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
280 CAAAAAGACCTTTAGAAGATGGAGATCAACACAGATGCTAAGAAAGTTGC 329
174 uGlyGlnArgGlySerSerArgGlnGlySerProGlySerValSerLysG 191
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
330 TCCTCAAAATGACTCTTTTGGACACAGTTACCA...CCGATGCATCAGC 376
191 lnLysProCysAspLeuProLeuArgLeuLeuValProThrGlnPheVal 207
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 AGCAAGATCTGTAATGACACAGAAATACAAAGTTCAGATGGAATGCTT 426
208 GlyAlaIlelleGlyLysGluGlyAlaThrIleArgAsnIleThrLysG1 224
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
427 GGATTCAATTTGGCAGAGGAGTCAACAGATCTCACGCATACACAGGA 476
224 nThrGlnSerLysIleAspValHisArgLysGluAsnAlaGlyAlaAlaG 241
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
477 ATCTGGATGCANAATACAGATA...GCTCTGACAGTGGTGGCTTCCAG 523
241 luLysSerIleThrIleLeuSerThrProGluGlyThrSerAlaAlaCys 257
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
524 AAAGTCTCTGTATGTTAACTGGAACACCTGAATCTGTCACGTCAGCAAAA 573
258 LysSerIleLeuGluIleMetHisLysGluAlaGlnAspIleLysPheTh 274
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
574 CGGTTACTGGACACAGATTGTTGAAAAAGGAAGACGAGCTCCTGGCTTCCA 623
274 rGlu.....GluIleProLeuLysIleLeuAlaHisAsnA 286
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
624 TCATGGCGATGGCGGAATGCGATTCAAGAAATCATGATTCAGCTA 673
286 snPheValIglyArgLeuIleGlyLysGluGlyArgAsnLeuLysLysIle 302
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
674 GCAAGCAGGAGTATTAGTCATTGGAAAAAGGGGAGAACTATTAAACAGCTT 723
303 GluGlnAspThrAspThrLysIleThrIleSerProLeuGlnGluLeuTh 319
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
724 CAGGAACGGCTGGAGTTAAATGTTATG.....ATTCAAGAC..... 762
319 rLeuTyrAsnProGluArgThr.....lleThrValLysG 331
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
763 .....GGGCGCGAGACACATGGTGTGACAAACCTCTTAGGATTACAG 805
331 lyAsnValGluThrCysAlaLysAlaGluGluIleMetLysLysIle 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
806 GAGACCCATATAAAGTTCAACACCAAGCAAGAAATGGTGTAGAGTTAATT 855
348 ArgGlu.....SerTyrGluAsnAspIleAlaSerMetAs 359

```



```
327 eThrValLysGlyAsnValGluThrCysAlaLysAlaGluGluIleM 344
      ::::::::::::::: ||| ||||| |||
1240 CACTGTGAGTGGAGAACCTGAACAAACCGAAAGCTGTGAACATTATCA 1289
      ||| ||| :::::::::::::::
344 eLysLysIleArgGlu.....Ser 350
      ::::::::::::::: |||
1290 TCCAGAAAGATACAAGAGGATCCACAAAGTGGCAGCTGTCTCAATATCAGT 1339
      ||| ||| :::::::::::::::
351 TyrGluAsn.....AspIleAlaSerMetAsn..... 359
      ||| ||| ::::::::::::::: |||
1340 TATGCCAATGTCACAGGTCACGTGGCAATTCCAATCCACCGGATCTCC 1389
      ||| ||| ::::::::::::::: |||
360 .....LeuGlnAlaHisL 364
      ||| ||| ::::::::::::::: |||
1390 TTATGCAACACTGCTGAAGTCTTACCAACTGCTGCAGCAGCTGCAGGC 1439
      ||| ||| ::::::::::::::: |||
364 euIleProGlyLeuAsnLeuAsnAlaLeuGlyLeuPheProThr... 379
      ||| ||| ||||| ::::::::::::::: |||
1440 TATTAGGACATGCTAACCTTGTCTGCGTGTGCAGCCTTTCCAGCAGTTTA 1489
      ||| ||| ::::::::::::::: |||
380 SerGlyMetProProThrSerGlyProProSerAlaMetThrProPr 396
      ||| ||| ::::::::::::::: |||
1490 TCTGGCTC.....ACAGGCAATGACCTGGTGGCCATCACCC..... 1525
      ||| ||| ::::::::::::::: |||
396 oTyrProGlnPheGluGlnSerGluThrGluThrValHisGlnPheIleP 413
      ||| ||| ::::::::::::::: |||
1526 .....TCTGCACCTTAATACATTA..... 1543
      ||| ||| ::::::::::::::: |||
413 roAlaLeuSerValGlyAlaIleIleGlyLysGlnGlyHisIleLys 429
      ||| ||| ||||| ::::::::::::::: |||
1544 .....GCCAGCTATGGTATATATCTCAACACTTTTAGGTTTAGGTCCTCAGT 1588
      ||| ||| ::::::::::::::: |||
430 GlnLeuSerArgPheAlaGlyAlaSerIleLysIleAlaProAlaGluAl 446
      ||| ||| ::::::::::::::: |||
1589 CAAGCAGCAGCA...ACAGGGCTTGGCTGCAGCAGCTGCAGTGCCNA 1635
      ||| ||| ::::::::::::::: |||
446 aProAspAlaLysValArgMetValIleIleThrGlyProProGluAlaG 463
      ||| ||| ::::::::::::::: |||
1636 CCCAGCAGCAGCAGCAGCAATTTATTTGGCCACCTATGCCAGTGAAGCT 1685
      ||| ||| ::::::::::::::: |||
463 InPheLys..... 465
      ||| ||| ::::::::::::::: |||
1686 CAGCCAGTGGCAGCAGCAGCTGTGTGACGGGGGACATTTGCATTAGGT 1735
      ||| ||| ::::::::::::::: |||
465 ..... 465
      ||| ||| ::::::::::::::: |||
1736 AGCCTGGCTGCTACTGCTGCACCAATGGATTTTGGAGCTGCTC 1785
      ||| ||| ::::::::::::::: |||
466 .....AlaGlnGlyArgIleTyrGlyLysIleLysGluGluAsnPheV 480
      ||| ||| ::::::::::::::: |||
1786 TCCCTCCTAGTGCACGTGCTTCTAGGA.....ACAGAAAAGTCCACAG 1829
      ||| ||| ::::::::::::::: |||
480 aLSerProLysGluGluValLysLeuGluAlaHisIleArgValProSer 496
      ||| ||| ::::::::::::::: |||
1830 ATGGATCCAAAGATAGTAGTAA.....ATAGCAGTGCAGAA 1867
      ||| ||| ::::::::::::::: |||
497 PheAlaAlaGlyArgValIleGlyLysGlyLysThrValAsnGluLe 513
      ||| ||| ::::::::::::::: |||
1868 NACTTAGTGGTGCATCTTGGCAAGAGGAGGAAACATTAGTGAATA 1917
      ||| ||| ::::::::::::::: |||
513 uGlnAsnLeuSerSerAlaGluValValProArg.....AspGlnT 528
      ||| ||| ::::::::::::::: |||
1918 CCAGGAGTTGACTGTGTGAAGGATACAGATCTCCAAAAAGAGAAATTCG 1967
      ||| ||| ::::::::::::::: |||
528 hrProAspGluAsnAspGlnValValLysIleThrGlyHisPheTyr 544
      ||| ||| ::::::::::::::: |||
1968 TACCTGGCAGCAGGAATCGAAGGTAAACC...ATTACTGGAAACACCACT 2014
      ||| ||| ::::::::::::::: |||
545 AlaCysGlnValAlaGlnArgLysIleGlnGluIleLeuThrGlnVal 561
      ||| ||| ::::::::::::::: |||
2015 GCACACAGGCTGCTCAATATTTAATTACACAAGGATCACAA..... 2056
      ||| ||| ::::::::::::::: |||
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```
561 sGlnHisGlnGlnLysAlaLeuGlnSerGlyProProGln 575
      ::::::::::::::: |||
2057 .....TATGACGAAGGAGTTGGGCTGCCAATCCTCAG 2089
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seq_name: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:US-60-278-232-11258

seq_documentation_block:
; Sequence 11258, Application US/60278232
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0011 P
; CURRENT APPLICATION NUMBER: US/60/278,232
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12,557
; SOFTWARE: PERL Program
; SEQ ID NO 11258
; LENGTH: 3316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 902614.14
; NAME/KEY: unsure
; LOCATION: 3256
; OTHER INFORMATION: a, t, c, g, or other
US-60-278-232-11258
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alignment_scores:
Quality: 217.50 Length: 534
Ratio: 0.853 Gaps: 26
Percent Similarity: 47.753 Percent Identity: 23.408

alignment_block:
US-09-466-396A-176 x US-60-278-232-11258 ..

Align seg 1/1 to: US-60-278-232-11258 from: 1 to: 3316

104 TyrGlyValValGluSerCysGluGln.ValAsnThrAspSerGluThrA 120
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457 TACTACTTTATTCTAGATTGCAGCCAAATTTGGGCGCATGCTGCCAGA 506
      ||| ||| ::||| ||| |||
120 laValValAsnValThr.....TyrSerSerLysAspGlnAlaArgGln 134
      ::||| ||| ||| ::||| ||| |||
507 CAGTGAATAACAGCACTCTGATTGTGTTTGGGGGCCAAAGAGACAG 556
      ||| ||| ||| ||| |||
135 AlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysVa 151
      ||| ||| ||| ||| |||
557 TTGGAGAT.....GGAGATCAACCGGAG.....AGCAAGAGCT 591
      ||| ||| ::||| ||| |||
151 AlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnP 168
      ||| ||| ::||| ||| |||
592 GCCTTCCCAGGGAGACTCAATCAGTTCTCAACTTGCACCCATCCATCC 641
      ||| ||| ::||| ||| |||
168 roArgGlyArgArgGlyLeuGlnArgGlySerSerArgGlnGlySer 184
      || ||| ||| |||
642 CC.....CCAAGGACTTCAATGACAGAA..... 664
      ||| ||| ::||| ||| |||
185 ProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu 201
      ||| ||| ::||| ||| |||
665 .....GAGTACAG 672
      ||| ||| ::||| ||| |||
201 uValProThrGlnPheValGlyAlaIleGlyLysGluGlyAlaThrI 218
      ||| ||| ::||| ||| |||
673 GGTCCACAGCAGCATGGTGGGCTGATCATTTGCAGAGGAGGTGAACAA 722
      ||| ||| ::||| ||| |||
218 leArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgLys 234
      ||| ||| ::||| ||| |||
```

723 TTAACAAATCCAAAGGATTACGGTGTCAAGATACAGATT...TCTCCA 769
235 GluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrProG1 251
770 GACAGGGTGGCTACCCAGCGCATGTGTCTTACAGAGGAGCCACAGA 819
251 uGlyThrSerAlaAlaCysLysSerIleLeuGluIleMet..... 264
820 ATCTGTCCAGAAAGCAAGATGATGTGTGATGACATTTGTCTCTCGGGGTC 869
265HisLysGluAla.....GlnAsp 270
870 GTGGGGGCCCCCAGGACAGTTCACAGCAACGCCAAGGGGGCCAGAAC 919
271 IleLysPheThrGluGluIleProLeuLysIleLeuAlaHisAsnAsnPh 287
920 GGCACCGTGCAGGAG.....ATCATGATCCCCCGGGCAA 954
287 eValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLysLysIleGluG 304
955 GCGCGGCTGGTCTTGGCAAGGGGGGAGACCATTAAGCAGCTGCAGG 1004
304 nAspThrAspThrLys...IleThrIleSerProLeuGlnGluLeuThr 319
1005 AACCGCTGAGTGAAGATCATCTTAATTCAGACGAGTCTCAGATACG 1054
320 LeuTyAsnProGluArgThrIleThrValLysGlyAsnValGluThrCy 336
1055AATGTGACAAACCTCTCCGATCATTTGGGGATCTTACAAAGT 1098
336 sAlaLysAlaGluGluIleMetLysLysIleArgGluSerTyArgGluA 353
1099 GCAGCAAGCTGTGAGATGGTGTGATGACATCTCCCGGGAACGTGACCAAG 1148
353 snAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsn 369
1149 GCGGCTTGGGACCGGATGATGATGATGATGATGATGATGATGATGATG 1192
370 LeuAsnAlaLeuGlyLeuPheProThrSerGlyMetProProTh 386
1193GCCATCATGTGCCA.. 1207
386 rSerGlyProProSerAlaMetThrProProTyProGlnPheGluGlnS 403
1207 1207
403 erGluThrGluThrValHisGlnPheIleProAlaLeuSerValGlyAla 419
1208GTGCCCAGGATCTGTGTGGGTG 1231
420 IleIleGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgPheAlaG1 436
1232 GTCATTTGGCGGAGTGAGAGATGATCAAGAAGATCCAGAATGATGCTGG 1281
436 yAlaSerIle.....LysIleA 442
1282 CGTGGGATACAGTTCAAGCAAGATGACGGGACAGGCGCCGAGAAAGATTG 1331
442 la.....ProAlaGluAlaProAspAlaLysValArgMetVal 454
1332 CTATATATATGGGCCCCCAGAGAGAGTGGCGAGCAGCAGCGCCGATCATC 1381
455IleIleThrGlyPro..... 460
1382 AACGACCTCTCCAGAGCTTCAGAGTGGTTCCTCCCGGAGTCTCCAGGGGG 1431
461GluAlaGlnPheLysAlaGlnGlyArgIleTyArgLysI 474
1432 TCCAGGCATCCCGGGGGGGCGAGCGCCGAGGAAGGAGGCAAGGC.... 1477
474 leLysGluGluAsnPheValSerProLysGluGluValLysLeuGluAla 490
1478AATGGGTGTCCTTGGGGGAGATGACCTTCTCC... 1513

491 HisIleArgValProSerPheAlaAlaGlyArgValIleGlyLysGlyG1 507
1514ATCCCACTCAAAAGTGTGGCTGTGTCATCGCGAGGTGG 1554
507 yLysThrValAsnGluLeuGlnAsnLeuSerSerAlaGluValValp 524
1555 CGAAGATGTGAAGCATAAACCCAGCAGACGGGAGCTTCGTAGATCT 1604
524 roArgAspGlnThrPro.....AspGluAsnAspGlnValValLys 538
1605 CCGGCGAGCTGCCACCCACGAGGGGCCCCCACTCAAGTTGTTTCATC... 1651
539 IleThrGlyHis.....PheTyAlaCysGlnValAlaGlnAr 551
1652 ATCCGGGTTTCAACCCAGCAGCATTTGACCGCAAGCAGCTTATCGAGGA 1701
551 gLysIleGlnGluIleLeu ThrGlnValLysGlnHisGlnGlnLys 567
1702 AAAGATCGAGGGTCTCTCTGCCCCAGTTGGACCGCCAGGTGGCCCG 1751
568 AlaLeu.....GlnSerGlyPro.....ProGlnSerArg 577
1752 GCCTGCTGCCCAATGGGGCCCTTCAATCTGGGCCCTTCAACCCAGG 1799
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seq_documentation_block:
Sequence 4435, Application US/60312544
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)A
CURRENT APPLICATION NUMBER: US/60/312,544
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 10730
SEQ ID NO 4435
LENGTH: 1852
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1725)
OTHER INFORMATION: Clone ID: LIB3205-293-H01_FLI
US-60-312-544-4435

alignment_scores:
Quality: 217.00 Length: 412
Ratio: 1.033 Gaps: 18
Percent Similarity: 50.971 Percent Identity: 23.786
alignment_block:
US-09-466-396A-176 x US-60-312-544-4435 ..
Align seg 1/1 to: US-60-312-544-4435 from: 1 to: 1852
193 ProCysAspLeuProLeuArgLeuLeuValProThrGlnPheValGlyAl 209
493 CTGGAGAGAGTGTTCGCCCATCTCTTCCAGCTCAGAGGTGGAGC 542
209 alleIleGlyLysGluGlyAlaThrIleArgAsnIleThrLysGlnThr 226
543 TATCATTTGGCCGCAAGGGAGTTTATCAAGAAGATGTGCGAGGAGACTA 592
226 lnSerLysIleAspValHisArgLysGluAsnAlaGlyAlaAlaGluLys 242
593 AAGCGGCATCAAAATA...CTTGATGGCCCACTGTGTGTACCAGAAAGA 639

```
243 SerIleThrIleLeuSerThrProGlu.....GlyThrSerAlaAl 526
   : : : : : ||| : : |||
640 GCAGTAATGATTTCAGCAAGGATGAACAGATGCACCTCTCTCTCCAGC 689
   : : : : : ||| : : |||
256 acylsYsserIleLeuGluIleMetHisLysGluAlaGlnaspIleLysP 273
   : : : : : ||| : : |||
690 TAGGATGGCTTACTTACGTAGAGTT...CATAAAGAATAACTGATAGTTCAG 736
   : : : : : ||| : : |||
273 heThrGluGluIle.....ProLeu 279
   : : : : : ||| : : |||
737 ATGCTGAATCTAGTCAACCTCAACCAAGTGTGGTAATATAGGACCAACA 786
   : : : : : ||| : : |||
280 LysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyLysGluCl 296
   : : : : : ||| : : |||
787 CGACTTCAGTCCATCTCTGCAAGCTGGCAGCCTTATTGGCAAGCAGGG 836
   : : : : : ||| : : |||
296 yArgAsnLeuLysLysIleGluGlnAspThrAspThrLysIleThrIleS 313
   : : : : : ||| : : |||
837 ACCAACTATTAAATCAATACAGATTTCTCAAAATCTATTGTCCGTATTG 886
   : : : : : ||| : : |||
313 erProLeuGlnGluLeuThrLeuTyAsnProGluArgThrIleThrVal 329
   : : : : : ||| : : |||
887 TTGACAATGTGCTCTCTGTTCCACTAAATGATGATAGAGTTGTGGAGATA 936
   : : : : : ||| : : |||
330 LysGlyAsnValGluThrCysAlaLysAlaGluGluGluIleMetLysLy 346
   : : : : : ||| : : |||
937 CAAGCGAGCCTCTTGGTGTCCAGGAAGCAGTGAATTAATATCGAGTCA 986
   : : : : : ||| : : |||
346 sIleArgGluSerTyGluAsnAspIleAlaSerMetAsnLeuGlnAlaH 363
   : : : : : ||| : : |||
987 CCTGAGAAATTTCTTGTGACCGCAGTGTTCACCATTTGTTGAAGCGC 1036
   : : : : : ||| : : |||
363 lsLeu...IleProGlyLeuAsnLeuAlaLeuGlyLeuPheProPro 378
   : : : : : ||| : : |||
1037 ATATGAAATGCGATGTATG.....CCGAGG 1062
   : : : : : ||| : : |||
379 ThrSerGlyMetProProThrSer...GlyProProSerAla...Me 393
   : : : : : ||| : : |||
1063 GAGCAACCAAGTCCACCTCCCGCAGTGGGGCCCTCTCTCAAACTGGAT 1112
   : : : : : ||| : : |||
393 tThrProPro.....TyrProG 399
   : : : : : ||| : : |||
1113 CCGCCCTCCAAACATCTCCAGGTGGTCTGGTTTGGAGAAATCCAC 1162
   : : : : : ||| : : |||
399 InPheGluGlnSerGluThrGluThrValHisGlnPheIleProAlaLeu 415
   : : : : : ||| : : |||
1163 ACTTCATGCATCCAGCGCGCAA.....GACAGTTACTATCTTCTCTCT 1206
   : : : : : ||| : : |||
416 SerValGlyAlaIleIleGlyLysGlnGlyGlnHisIleLysGlnLeuSe 432
   : : : : : ||| : : |||
1207 GATGTC.....CCCCATATGAAAGCAGCC 1232
   : : : : : ||| : : |||
432 rArgPheAlaGlyAlaSerIleLysIleAlaProAlaGluAlaProAspA 449
   : : : : : ||| : : |||
1233 GCACCTAC.....GGTATTCTGCATACGCCGGGAGGCCGCCCAAA 1273
   : : : : : ||| : : |||
449 laLysValArgMetValIleIleThrGly.....ProProGluAlaGln 463
   : : : : : ||| : : |||
1274 GTGGTGTCTCT.....GCTACAGGGAATCAACCACTCT..... 1308
   : : : : : ||| : : |||
464 PheLysAlaGlnGlyArgIleTyGlyLysIleLysGluGluAsnPheVa 480
   : : : : : ||| : : |||
1308 ..... 1308
   : : : : : ||| : : |||
480 lserProLysGluGluValLysLeuGluAlaHisIleArgValProSerP 497
   : : : : : ||| : : |||
1309 .CATCCAGTTCTCAGGTGGCTCATGCATGCACATT.....CCCTTG 1351
   : : : : : ||| : : |||
497 heAlaAlaGlyArgValIleGlyLysGlyGlyLysThrValAsnGluLeu 513
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1352 CCTACCGCTGATGCTGTGATTGGGCGAGCTGGTGTGCTAGTATCATCATC 1401
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2001, 06:22:32 ; Search time 4669.91 Seconds
(without alignments)
13229.772 Million cell updates/sec

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Perfect score: 4181
Sequence: 1 99tggatgcgtttgggtgtt.....aaaaaaaaaaaaaaaaaaaaa 4181

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues
Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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2: /cgn2_6/ptodata/2/pna/US06_COMB.seq.*
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43: /cgn2_6/ptodata/2/pna/US09811_COMB.seq.*

44: /cgn2_6/ptodata/2/pna/US6012_COMB.seq.*
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57: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
58: /cgn2_6/ptodata/2/pna/US6026_COMB.seq.*
59: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
60: /cgn2_6/ptodata/2/pna/US6028_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4165	99.6	4181	18	US-09-466-396A-175 Sequence 175, App
2	4165	99.6	4181	21	US-09-543-615A-175 Sequence 175, App
3	4165	99.6	4181	23	US-09-606-421A-175 Sequence 175, App
4	4165	99.6	4181	24	US-09-630-940A-175 Sequence 175, App
5	4165	99.6	4181	25	US-09-643-597-175 Sequence 175, App
6	4165	99.6	4181	26	US-09-662-786-175 Sequence 175, App
7	4165	99.6	4181	27	US-09-685-696-175 Sequence 175, App
8	4165	99.6	4181	29	US-09-735-705-175 Sequence 175, App
9	4165	99.6	4181	31	US-09-850-716-175 Sequence 175, App
10	4165	99.6	4181	31	US-09-850-716-175 Sequence 175, App
11	4143	99.1	4159	14	US-09-061-709-4 Sequence 4, Appli
12	4143	99.1	4159	16	US-09-270-437-4 Sequence 4, Appli
13	3990.8	95.5	4434	60	US-60-281-593-145 Sequence 145, App
14	3987	95.4	4430	49	US-60-172-360-28769 Sequence 28769, A
15	1736.8	41.5	1740	21	US-09-543-615A-347 Sequence 347, App
16	1736.8	41.5	1740	23	US-09-606-421A-347 Sequence 347, App
17	1736.8	41.5	1740	24	US-09-630-940A-347 Sequence 347, App
18	1736.8	41.5	1740	25	US-09-643-597-347 Sequence 347, App
19	1736.8	41.5	1740	26	US-09-662-786-347 Sequence 347, App
20	1736.8	41.5	1740	27	US-09-685-696-347 Sequence 347, App
21	1736.8	41.5	1740	29	US-09-735-705-347 Sequence 347, App
22	1736.8	41.5	1740	31	US-09-850-716-347 Sequence 347, App
23	1736.8	41.5	1740	31	US-09-850-716-347 Sequence 347, App
24	1734.2	41.5	1764	31	US-09-850-716-428 Sequence 428, App
25	1700.8	40.7	1983	17	US-09-396-087-4542 Sequence 4542, Ap
26	1330.4	31.8	1764	25	US-09-644-869-7957 Sequence 7957, Ap
27	1330.4	31.8	1764	25	US-09-652-109-8549 Sequence 8549, Ap
28	1012.2	24.2	1160	55	US-60-236-804-331 Sequence 331, App
29	820.4	19.6	2512	23	US-09-617-182-2240 Sequence 2240, Ap
30	744	17.8	843	17	US-09-399-932-4493 Sequence 4493, Ap
31	720	17.2	834	25	US-09-652-123-8442 Sequence 8442, Ap
32	710.4	17.0	3374	1	PCT-US01-01307-1113 Sequence 113, App
33	710.4	17.0	3412	14	US-09-061-709-6 Sequence 6, Appli
34	710.4	17.0	3412	16	US-09-270-437-6 Sequence 6, Appli
35	699.4	16.7	3650	1	PCT-US01-01341-3275 Sequence 329, App
36	699.4	16.7	3650	49	US-60-172-360-27652 Sequence 27652, A
37	695.6	16.6	3283	14	US-09-061-709-8 Sequence 8, Appli
38	695.6	16.6	3283	16	US-09-270-437-8 Sequence 8, Appli
39	695.6	16.6	3896	25	US-09-644-869-8906 Sequence 8906, Ap
40	695.6	16.6	3896	27	US-09-699-998-9743 Sequence 9743, Ap
41	695.6	16.6	3896	29	US-09-721-589-6556 Sequence 6556, Ap
42	672.6	16.1	1946	14	US-09-061-709-7 Sequence 7, Appli
43	672.6	16.1	1946	16	US-09-270-437-7 Sequence 7, Appli
44	580.6	13.9	1708	14	US-09-061-709-5 Sequence 5, Appli
45	580.6	13.9	1708	16	US-09-270-437-5 Sequence 5, Appli

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RESULT 5
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; Sequence 175, Application US/09630940B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367

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RESULT 9
US-09-735-705-175
; Sequence 175, Application US/09735705
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: 210121.455C14
; REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure

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nnlication iis/09735705

: GENERAL INFORMATION.

APPLICANT: Wang. Tonatong

APPLICANT: Fan, Liang

APPLICANT: Kallos, Michael D.

; APPLICANT: Banpur, Chaita

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
PREPARATION AND DETECTION OF FINE GRAIN; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 010101455014

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; FILE REFERENCE: 210121.455C14
CURRENT ADDITION: NEWTON - 10

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; CURRENT APPLICATION NUMBER: US/09/133,703
 ; CURRENT FILING DATE: 2000-12-12

; CURRENT FILING DATE: 2000-12-12
 : NUMBER OF SEC ID NOS: 418

; NUMBER OF SEQ ID NOS. 413
; SOFTWARE: FastSeq for Windows Version 3.0: SOFIWAKL: FB
: SEO ID NO 175

: LENGTH: 4181

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TYPE: DNA

: : ORGANTSM: Homo sapiens

FEATUFE:

NAME/KEY: unsure

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RESULT 12

RESOLI 12
US-09-270-437-4

03 03 270 437 4
; Sequence 4, Application US/09270437A

; GENERAL INFORMATION:

; APPLICANT: Chen, Yao-Tseng

APPLICANT: Gure, Ali

; APPLICANT: Tsang, Solam

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Jager, Elke

APPLICANT: Knuth, Alexander

; APPLICANT: Old, Lloyd J

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Ant

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RESULT 14
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; Sequence 28769, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 28769
; LENGTH: 4430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 236315.6
; NAME/KEY: unsure
; LOCATION: 2204, 2212, 2216, 2222
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-360-28769

Query Match          95.4%; Score 3987; DB 49; Length 4430;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 4090; Conservative 0; Mismatches 50; Indels 15; Gaps 7;

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Search completed: September 29, 2001, 10:03:56
Job time: 13284 sec

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2	3865.6	92.5	4264	1	PCR-US01-08631-21954	Sequence 21954, A
3	1837	43.9	1985	1	PCR-US01-08631-12583	Sequence 12583, A
4	710.4	17.0	2010	1	PCR-US01-08631-6785	Sequence 6785, Ap
5	695.6	16.6	3667	1	PCR-US01-08631-6786	Sequence 6786, Ap
6	409.6	9.8	583	5	US-09-510-376A-100	Sequence 100, Appl
7	324.6	7.8	456	1	PCR-US01-08631-21953	Sequence 21953, A
8	237.2	5.7	516	6	US-60-253-652-10626	Sequence 10626, A
9	231.4	5.5	321	4	US-08-798-0748-12440	Sequence 12440, A
10	231.4	5.5	321	4	US-08-798-0748-12440	Sequence 12440, A
11	231.4	5.5	321	4	US-08-798-074C-12440	Sequence 12440, A
12	225.2	5.4	315	1	PCR-US01-08631-21951	Sequence 21951, A
13	184.4	4.4	305	5	US-09-842-827-1757	Sequence 1757, Ap
14	173.2	4.1	383	6	US-60-253-652-6909	Sequence 6909, Ap
15	170.2	4.1	1998	1	PCR-US01-08631-12584	Sequence 12584, A
16	169.6	4.1	273	6	US-60-253-653-21454	Sequence 21454, A
17	167.8	4.0	1998	1	PCR-US01-08631-21952	Sequence 21952, A
18	76.4	1.8	102	6	US-60-253-653-16840	Sequence 16840, A
19	60.8	1.5	65	6	US-60-287-724-25276	Sequence 25276, A
20	60	1.4	60	6	US-60-287-724-15603	Sequence 15603, A
21	60	1.4	60	6	US-60-287-724-31874	Sequence 31874, A
22	53.8	1.3	60	6	US-60-287-724-31746	Sequence 31746, A
23	53.8	1.3	60	6	US-60-287-724-31875	Sequence 31875, A
C 24	53.6	1.3	2328	5	US-09-825-732-1564	Sequence 1564, Ap
C 25	52.8	1.3	860	5	US-09-824-557-79	Sequence 79, Appl
C 26	47.8	1.1	394	5	US-09-824-557-2211	Sequence 2211, Ap
C 27	47	1.1	530	5	US-09-824-557-4903	Sequence 4903, Ap

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Qy 2461 gttttatttttccctaaacactacatgagttaacctaaaggggaggtgtgaaagggtgtggc 2520

Db	3541	ggacata	nttata	ccccctt	taaaaaaaa	ccccctg	ccctcattcttattt	cgagatga	3600
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Db	3601	attcgata	cagactaga	tgtcttctg	aaagatcaat	tagacat	ntngaaaatgatttaa	3660	
Qy	3661	agtg	ttttt	ctctaagt	tctctg	aaaaa	caagttctctttgtagttttta	ccccaaaaagtg	3720
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Qy	3721	ccct	ttttg	tgcactg	gtttctctc	tagcattcaat	gatttttttttccacacaaatgaattaaa	3780	
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RESULT 2
PCT-US01-08631-21954
; Sequence 21954, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc

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: APPLICANT: Hyseq, Inc
:
: TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
:
: FILE REFERENCE: 21272-049
:
: CURRENT APPLICATION NUMBER: PCT/US01/08631
:
: CURRENT FILING DATE: 2001-03-30
:
: PRIOR APPLICATION NUMBER: 09/540,217
:
: PRIOR FILING DATE: 2000-03-31
:
: PRIOR APPLICATION NUMBER: 09/649,167
:
: PRIOR FILING DATE: 2000-08-23
:
: NUMBER OF SEQ ID NOS: 60736
:
: SOFTWARE: Custom
:
: SEQ ID NO 21954
:
: LENGTH: 4264
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: SIMILAR
:
: LOCATION: (1774)..(2013)
:
: OTHER INFORMATION: 55% homologous to Homo sapiens IGF-1
:
: OTHER INFORMATION: 3,accession number AF117108,Smith-Wa
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: PCT-US01-08631-21954

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Query Match 92.5%; Score 3865.6; DB 1; Length 4264;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 4090: Conservative 0; Mismatches 60; Indels 28;

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RESULT 3
PCT-US01-08631-12583
; Sequence 12583, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217

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; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 12583
; LENGTH: 1985
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (164)..(3)
; OTHER INFORMATION: 79% homologous to Homo sapiens Human secreted protein
; OTHER INFORMATION: HLYE538, SEQ ID NO:220,accession number Y86305,Smith-Waterman Seq
; OTHER INFORMATION: -211.
PCT-US01-08631-12583

Query Match      43.98; Score 1837; DB 1; Length 1985;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1915; Conservative 1; Mismatches 57; Indels 14; Gaps 3;

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Qy 311 atcttcaggagcgcgaagatccccggtgtcgggaccccttcctcgtgaagactggctacgcg 370
Db atcttgaaggacgcgaagatccccggtgtcgggaccccttcctcgtgaagactggctacgcg 120

Qy 371 ttcgtgactccggacgagatgtggccctcgaagccatcgaagcgttcctcgggttaa 430
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Qy 431 atgaactgcacgggaaacccatagaaagttagcactcgtcccaaaaaggcaagatt 490
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Qy 491 cggaacttcagatcacgaatatccccctcatttacagtgggaggtcgtggatagttta 550
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Qy 611 gttgtaaatgtaacctattccagtaaggaccacaa-----gctagacaaagcactag 659
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Qy 720 aaatggccgcgcagcaaaaccccttcagacagcccgaggtcgcggggcttggcaga 779
Db 481 aaatggccgcgcagcaaaaccccttcagacagcccgaggtcgcggggcttggcaga 540

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Qy 1020 gtaagtctattctggagattatgcataaggagctcaagatatataaaattcacagaaga 1079
Db 781 gtaagtctattctggagattatgcgtaaggaaactcaagatgtaaaattcacagaaga 840

Qy 1080 tcccttgaagatttttagctcataataaactttgttgacgtctctattggtaaaagaaga 1139
Db 841 tcccttgaagatttttagctcaaaataaactttgttgccgtctctattggtaaaagaaga 900

Qy 1140 gaaatcttaaaaaaatiagcaacagacacagacactaaatacacgatatctccattgcagg 1199
Db 901 gaaatcttaaaaaaatiagcaacagacacactaaatacacgatatctccattgcagg 960

Qy 1200 aattgacgtgtataatccagaaacgcctatttacagtttaaaggccaattgttgagacatgt 1259
Db 961 aactgatgcagtataatccagaaacacacacattacagctaaaggccaattgttgagacatgt 1020

Qy 1260 ccaagctggaggagagatcatgaagaaaatcaggggagctctatgaaaaatgatattgctt 1319
Db 1021 ccaagctggaggagagatcatgaagaaaatcaggggagcttaggaaaatgatattcactt 1080

Qy 1320 ctatgaatcttcaagcacatttaattcctgattaaatctgaacgccttgggtctgttccc 1379
Db 1081 ctatga--tttcaagcacatttaattcctgattaaatctgaacgccttgggtctgttccc 1138

Qy 1380 caccacttcagggtatgccactccacactcaggggccccccttcaggccatgactcctccc 1439
Db 1139 caccacttcagggtatgccactccacactcaggggccccccttcaggccatgactcctccc 1198

Qy 1440 accgcagtttgagcaatcagaaacggagactgttcatcagtttatcccaagctctatacg 1499
Db 1199 cccgcagtttgagcaatcagaaatcccagactgttcatctgtttatcccggtctatacg 1258

Qy 1500 tcggtgcactcatcgcaagcagggccagcacatcaagcagcttctcgccttgcctgagag 1559
Db 1259 tcagagccctcatcagcaagcagggccagcacatcaagcagcttctcgccttgcctgagag 1318

Qy 1560 cttaaatgaagattgtccagcggaagcaccagatgctaaagtgagatggtgtgattatca 1619
Db 1319 cttaaatgaagattgtccagcggaagcaccagatgctaaagtgagatggtgtgattatca 1378

Qy 1620 ctggaccacacagagctcagttcaagctcagggaagaatttatggaaaaataaagaag 1679
Db 1379 ctggaccacacagagctcagttcaagctcagggaagaatttatggaaaaataaagaag 1438

Qy 1680 aaaaactttagtctcctaaagaagagtgaaacttgaagctcatatcagagtgccatcct 1739
Db 1439 aaaaactttagtctcctaaagaagagtgaaacttgaagctcatatcagagtgccatcct 1498

Qy 1740 ttgctgtggaaggttatttgaaaaagggaacacgggtgaatgaaacttcagaatttgt 1799
Db 1499 ttgctgtggaaggttatttgaaaaagggaacacgggtgaatgaaacttcagaatttgt 1558

Qy 1800 caagtgcagaagttgttccctcgtgaccagacacacacacacacacacacacacacacac 1859
Db 1559 caagtgcagaagttgttccctcgtgaccagacacacacacacacacacacacacacacac 1618

Qy 1860 tcaaaaataactggttcacttctatgttgcaggttgcacagagaaaaatccaggaatcc 1919
Db 1619 tcaaaaataactggttcacttctatgttgcaggttgcacagagaaaaatccaggaatcc 1678

Qy 1920 tgactcgggttaagcagcaccaacacacagaggtcctgcgaagtggaccacctcagtcac 1979
Db 1679 tgactcgggttaagcagcaccaacacacagaggtcctgcgaagtggaccacctcagtcac 1738

Qy 1980 gacggaagttaaggctcagaaacacacacacacacacacacacacacacacacacacac 2039
Db 1739 gacggaagttaaggctcagaaacacacacacacacacacacacacacacacacacacac 1798*

Qy 2040 atgcttaacaaacagatggcgctgacccctctatccagaaatcagatgcacaaagttttta 2099
Db 1799 atgcttaacaaacagatggcgctgacccctctatccagaaatcagatgcacaaagttttta 1858
```


QY 2100 cctagccagttgttcttctgagaccaggaacactttttgaact-cctgtctctctgtgagaatgt 2158
|||||
Db 1859 cctagccagttgttcttctgagaccaggaacacttttgaactcctctgtctctgtgagaatgt 1918
QY 2159 atactttatgtctctgaaatgtatgacaccagcttttaaaacaaacaaacaaacaaacaa 2218
|||||
Db 1919 atactttatgtctctgaaatgtatgacaccagcttttaaaacaaacaaacaaacaaacaa 1978
QY 2219 aaaaaa 2225
|||||
Db 1979 aaaaaa 1985

RESULT 4

PCT-US01-08631-6785
; Sequence 6785, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; PRIORITY FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 6785
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (50)..(1843)
; OTHER INFORMATION: 100% homologous to Homo sapiens IGF-II mRNA-binding protein
; OTHER INFORMATION: 2, accession number AF117107, Smith-Waterman Score=3059.
PCT-US01-08631-6785

Query Match 17.0%; Score 710.4; DB 1; Length 2010;
Best Local Similarity 64.5%; Pred. No. 1.2e-129;
Matches 1155; Conservative 0; Mismatches 556; Indels 81; Gaps 3;

QY 251 atgaacaaactgtatatcggaacactcagcagagaacgcgcgcctcccgacactagaaagt 310
|||||
Db 50 atgaacaaactgtatatcggaacactcagcagagaacgcgcgcctcccgacactcgcgcgca 109
QY 311 atcttcaaggacgcgaagatcccggtgtctgaggacacttctctgtggaactggtctacgcg 370
|||||
Db 110 ctcttggggacagaagctgcctctggcgacaggtctctgtgaagtcccggtctacgc 169
QY 371 ttcgtgactcgcgcgacagagctggccctcaaggcctcagcagcagcgtcttcaggtaaa 430
|||||
Db 170 ttcgtgactcgcgcgacagagctggccctcaaggcctcagcagcagcgtcttcaggtaaa 229
QY 431 atagaactgcacgcgggaaccccaatagaagttagcactcgttcccaaaaggcaaggatt 490
|||||
Db 230 gfggaattgcattggaataatcaggaattgattactcagctctctaaaaagctaaaggagc 289
QY 491 cggaaacttcagatcagaaataatccgcctcatttacagtgaggaggtgctgatatgttta 550
|||||
Db 290 aggaataatcagatcagaaataatccgcctcatttacagtgaggaggtgctgatatgttta 349
QY 551 ctagtccagtagtgagtgagagcgtgagcaagtgaacactgactcggaaactgca 610
|||||
Db 350 tgggtccaatatggacagtgagagatgtggcaacagtcacacacagacacagaacccgcc 409
QY 611 gttgtaaatgtaacctattccagtaggaacaaagctagacaagcactgacacaaactgaat 670
|||||
Db 410 gttgtaaatgtaacctattccagtaggaacaaagctagacaagcactgacacaaactgaat 469
QY 671 ggaatttcagtaggaatttcaccttgaagttagcctatatccctgatgaaatggccgcc 730

Db 470 gggaatcagtttgagaactactccttcaagatttctcatctcccgatgaagagtgcagc 529
QY 731 cagcaaaaccccttcagcagcccgaggtgcgcggggttggcagaggggtccctca 790
|||||
Db 530 tcccttcgccccctcagcagcccgagcgtggggaccactcttccgggagcaaggccac 589
QY 791 aggcagggttccaggatccgtaaccaagcagaaccatgtgatttgcctctgcctcg 850
|||||
Db 590 g-----cccttggggcaacttctcaggccagacagattgatttcccgctcggaac 640
QY 851 ctggttcccaacccaatttgttgagccatcatagaaagaagggtgccacatttcggaaac 910
|||||
Db 641 ctggttcccaacccaatttgttgagccatcatcgaaaggaggttgcacataaagaac 700
QY 911 atcacaacacagaccagctctaaatcagatgccaccgttaaagaaaatgcggggctgt 970
|||||
Db 701 atcactaagcagaccagctcccggttagatataccatagaaaagagaactcttgagctgca 760
QY 971 gagaagtcgattactctctctactctgaagcactctgcggttgcgttgaagtctatt 1030
|||||
Db 761 gagaagcctgtcaccatccatgcccccagagggactcttgaagcatgccgcgatgatt 820
QY 1031 ctggagattatgcataaagaagctcaagatatataaattcacagaagagatcccttgaag 1090
|||||
Db 821 ctggaatcatgcagaagaagcagatgagaccaaactagccgaagagagattctctgaaa 880
QY 1091 attttagctcataataaactttgtgagcgtcttattgttaaagaaggaagaactcttaaa 1150
|||||
Db 881 atcttggcaccaatgtggttggtagactgattggaagaaggagccgaatttgaag 940
QY 1151 aaaaattgagcagacacagacactaaaatcacgatatctccatttcagaaattgcagctg 1210
|||||
Db 941 aaaaattgacatgaacaggggacaaagataaacaattctcatcttgcagatttgagcata 1000
QY 1211 tataatcagaacgcactattacagttaaagcaatgttgagacatgtgtcccaaaagctgag 1270
|||||
Db 1001 tacaacccggaaagaacactcactgtgaaggcagctgtgagcctgtgagcctgtgagcag 1060
QY 1271 gaggagatcatgaagaaaatcaggagcttattatgaaaatgatattgcttctatgaatt 1330
|||||
Db 1061 atagagattatgaagaagcgtgcgtgagccttgaagaatgatattgctgttaacaa 1120
QY 1331 caagcacaatttaattctctggattaaatcgaacgctgtggtctgttcccaacccactca 1390
|||||
Db 1121 caagcacaattctgatcccggttgaacctcagcacttggcatcttttcaacaggactg 1180
QY 1391 gggatgcacactccacactcaggggcccttcagcactgactcct----- 1435
|||||
Db 1181 tccgtgctatctccacagcaggcccgcgagctcccccgcgtgcccccctaccacccc 1240
QY 1436 -----ccctaccgcagtttgagc----- 1454
|||||
Db 1241 ttcaataccacactccggataacttctccagctgtaccoccatcaccagtttggcccgcttc 1300
QY 1455 -----aatcagaacggagagctgttcacagtttatccagctctatca 1498
|||||
Db 1301 ccgcatcatcactcttaccagcaggagattggaatctctctatcccaacccaggtc 1360
QY 1499 gtcgtgccaatcatcggcaagcaggccacacatacgaacagcttctcgttctgtgga 1558
|||||
Db 1361 gtcgtgccaatcatcggcaagcaggccacacatacgaacagctggtgagattcgcggga 1420
QY 1559 gcttcaattaaagatgctccagcaggaagcaccagatgctaaagtggaggtggtgattc 1618
|||||
Db 1421 gctctataaagattgccccctcggaagccacagcgtcagcgaaggatggtcatcacc 1480
QY 1619 actgaccacccagcgtcagttcaggctcagggaagaatttatggaaaaataaagaa 1678
|||||
Db 1481 accggccaccggaaagcccgatcgaagcccgagcgtcttgggaaactgaaagag 1540
QY 1679 gaaaacttggtagtctctaaagaaggtgaaactggaagctcatcatcagatggccatcc 1738
|||||

Db	1541	gaaaactctttaaccccaaaagaagaagtgaagctggaagcgcatatacgaagtgcctct	1600
Qy	1739	tttgctgctggcagagttatttgaaagagagcgcaaacggtgaatgaacttcagaattg	1798
Db	1601	tccacagctggccgggtgatggcaaaagtggcaagaccgtgaacgaactgcagaacta	1660
Qy	1799	tcaagtgcagaagttgtcttcctcgtgaccacagacacctgtagaatagccaaagtgtt	1858
Db	1661	accagtgcaagatcatcgtgctcgtgaccaaacgcagatgaatgggaagtgtc	1720
Qy	1859	gtcaaaataactgtgcactctctatctgtgccaggtgccacagaaaaattcaggaaatt	1918
Db	1721	gtcagaattatcgggcactctcttctgacgacactgcacagcgcaagatcaggggaaatt	1780
Qy	1919	ctgactcaggtaaagcagcaccacaaacagaaggtctgtcaaatggaccac	1970
Db	1781	gtacaacagttgaagcagcagagcagaaaaatccctcaggaagtgcgctcac	1832

RESULT 5

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PCT-US01-08631-6786
; Sequence 6786, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540, 217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 6786
; LENGTH: 3667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (436)..(2103)
; OTHER INFORMATION: 100% homologous to Homo sapiens hepatocellular carcinoma
; OTHER INFORMATION: autoantigen,accession number AF057352,Smith-Waterman Score=2838
PCT-US01-08631-6786

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Query Match	16.6%	Score 695.6	DB 1	Length 3667
Best Local Similarity	64.8%	Pred. No. 1e-126		
Matches 1115; Conservative	0	Mismatches 539	Indels 66	Gaps 3

[illegible]


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; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 12584
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (3)..(1469)
; OTHER INFORMATION: 31% homologous to Herpesvirus papio NTR, accession number
; OTHER INFORMATION: AF200364, Smith-Waterman Score=247.
PCT-US01-08631-12584

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Query Match          4.1%; Score 170.2; DB 1; Length 1998;
Best Local Similarity 98.3%; Pred. No. 2.9e-24;
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1811 gttgtgtccctcgtagccagacacctgatgagaatgaccgaagtgtgtgtcaaaaataact 1870
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 462 ggtgtgtccctcgtagccagacacctgatgagaatgaccgaagtgtgtgtcaaaaataact 521

QY 1871 ggtcacttctatgcttgccaggttgccagagagaaaaattcaggaaaattctgactcaggta 1930
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 522 ggtcacttctatgcttgccaggttgccagagagaaaaattcaggaaaattctgactcaggta 581

QY 1931 aagcagcaccacaacagagaaggtctgtcaaatggaccacctcagtcacagacgga 1985
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 582 aagcagcagcaacaacagagaaggtctgtcaaatggaccacctcagtcacagacgga 636

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Search completed: September 29, 2001, 10:05:25
Job time: 10768 sec

